

GenCore version 5.1.6  
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nucleic - nucleic search, using sw model

on: November 8, 2003, 01:25:59 ; Search time 244 Seconds  
(without alignments)

274.632 Million cell updates/sec

let: US-09-944-326-4

fact score: 21

fluence: 1 cagcagcagctctcatcat 21

ring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

urched: 2141354 seqs, 1595478879 residues

al number of hits satisfying chosen parameters: 4282708

imum DB seq length: 0

imum DB seq length: 200000000

ic-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

abase : Published Applications NA:\*

1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*

3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*

4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*

6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*

8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*

11: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*

12: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*

13: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*

14: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*

15: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*

16: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

ult No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	10	US-09-944-326-4
2	21	100.0	21	12	US-09-967-726A-4
3	21	100.0	21	12	US-10-080-794-4
4	21	100.0	396	9	US-09-825-284-15
5	21	100.0	396	10	US-09-970-866-15
6	21	100.0	396	15	US-10-212-677-15
7	21	100.0	461	11	US-09-918-995-32172
8	21	100.0	462	11	US-09-918-995-2524
9	21	100.0	465	11	US-09-918-995-32177
10	21	100.0	490	11	US-09-918-995-12511
11	21	100.0	491	11	US-09-918-995-17455
12	21	100.0	492	10	US-09-918-995-31156
13	21	100.0	532	10	US-09-833-381-910
14	21	100.0	1451	12	US-10-133-013-214
15	21	100.0	1614	12	US-10-119-428-31
16	21	100.0	1678	10	US-09-765-231A-16

C 17	21	100.0	1775	12	US-10-133-013-243	Sequence 243, App
C 18	20	95.2	277	10	US-09-833-381-1241	Sequence 1241, Ap
C 19	19.4	92.4	123	10	US-09-783-590-3282	Sequence 3282, Ap
C 20	19.4	92.4	539	11	US-09-918-995-31688	Sequence 31688, A
C 21	17.8	84.8	21	12	US-09-967-726A-15	Sequence 15, App1
C 22	17.8	84.8	21	12	US-10-080-794-15	Sequence 15, App1
C 23	17.8	84.8	366	10	US-09-960-352-188	Sequence 188, App
C 24	17.8	84.8	377	10	US-09-960-352-3858	Sequence 3858, App
C 25	17.8	84.8	379	10	US-09-960-352-6621	Sequence 6621, Ap
C 26	17.8	84.8	389	10	US-09-960-352-14093	Sequence 14093, A
C 27	17.8	84.8	413	10	US-09-960-352-2490	Sequence 2490, Ap
C 28	17.8	84.8	414	10	US-09-960-352-2489	Sequence 2489, Ap
C 29	17.8	84.8	414	10	US-09-960-352-10772	Sequence 10772, A
C 30	17.8	84.8	416	10	US-09-960-352-8509	Sequence 8509, Ap
C 31	17.8	84.8	426	10	US-09-960-352-6031	Sequence 6031, Ap
C 32	17.8	84.8	462	12	US-10-027-632-292190	Sequence 292190,
C 33	17.8	84.8	462	13	US-10-027-632-292190	Sequence 292190,
C 34	17.8	84.8	2239	12	US-10-027-632-111116	Sequence 111116,
C 35	17.8	84.8	2239	12	US-10-027-632-111117	Sequence 111117,
C 36	17.8	84.8	2239	13	US-10-027-632-111116	Sequence 111116,
C 37	17.8	84.8	2239	13	US-10-027-632-111117	Sequence 111117,
C 38	17.4	82.9	300	10	US-09-941-997-1	Sequence 1, App1
C 39	17.4	82.9	379	11	US-09-918-995-3393	Sequence 3393, App
C 40	17.4	82.9	396	11	US-09-918-995-3872	Sequence 3872, Ap
C 41	17.4	82.9	407	11	US-09-918-995-2976	Sequence 2976, Ap
C 42	17.4	82.9	415	11	US-09-918-995-5801	Sequence 5801, Ap
C 43	17.4	82.9	441	11	US-09-918-995-3798	Sequence 3798, Ap
C 44	17.4	82.9	455	11	US-09-918-995-5994	Sequence 5994, Ap
C 45	17.4	82.9	481	11	US-09-918-995-4221	Sequence 4221, Ap

## ALIGNMENTS

RESULT 1  
US-09-944-326-4  
Sequence 4, Application US/09944326  
Patent No. US20020128220A1  
GENERAL INFORMATION:  
APPLICANT: Gleave, Martin  
APPLICANT: Rennie, Paul S.  
APPLICANT: Miyake, Hideaki  
APPLICANT: Nelson, Colleen  
TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY  
FILE REFERENCE: UBC P-020-2  
CURRENT APPLICATION NUMBER: US/09/944,326  
CURRENT FILING DATE: 2001-08-30  
PRIOR APPLICATION NUMBER: 60/121,726  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 09/913,325  
PRIOR FILING DATE: 2001-08-10  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 21  
TYPE: DNA  
ORGANISM: HUMAN  
FEATURE:  
OTHER INFORMATION: antisense TRPM-2 ODN  
US-09-944-326-4

Query Match 100.0%; Score 21; DB 10; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CAGCAGCAGCTCTCATCAT 21  
Db 1 CAGCAGCAGCTCTCATCAT 21

RESULT 2  
US-09-967-726A-4  
Sequence 4, Application US/09967726A

Publication No. US20030158130A1  
GENERAL INFORMATION:  
APPLICANT: Gleave, Martin  
APPLICANT: Rennie, Paul S.  
APPLICANT: Miyake, Hideaki  
APPLICANT: Nelson, Colleen  
APPLICANT: Zellweger, Tobias  
TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2  
FILE REFERENCE: UBC-P-022  
CURRENT APPLICATION NUMBER: US/09/967,726A  
CURRENT FILING DATE: 2001-09-28  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Version 3.1  
SEQ ID NO 4  
LENGTH: 21  
TYPE: DNA  
ORGANISM: human  
US-967-726A-4  
Query Match  
Best Local Similarity 100.0%; Score 21; DB 12; Length 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 CAGCAGCAGAGCTTTCATCAT 21  
1 CAGCAGCAGAGCTTTCATCAT 21  
LT 3  
US-080-794-4  
Sequence 4, Application US/10080794  
Publication No. US20030165591A1  
GENERAL INFORMATION:  
APPLICANT: Gleave, Martin  
APPLICANT: Rennie, Paul S.  
APPLICANT: Miyake, Hideaki  
APPLICANT: Nelson, Colleen  
APPLICANT: Monia, Brett P.  
TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE  
FILE REFERENCE: UBC-P-020-3  
CURRENT APPLICATION NUMBER: US/10/080,794  
CURRENT FILING DATE: 2002-02-22  
RIOR APPLICATION NUMBER: 60/121,726  
RIOR FILING DATE: 1999-02-26  
RIOR APPLICATION NUMBER: 09/913,325  
RIOR FILING DATE: 2001-08-10  
RIOR APPLICATION NUMBER: 09/944,326  
RIOR FILING DATE: 2001-08-30  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 21  
TYPE: DNA  
ORGANISM: HUMAN  
FEATURES:  
OTHER INFORMATION: antisense TRPM-2 CDN  
US-080-794-4  
Query Match  
Best Local Similarity 100.0%; Score 21; DB 12; Length 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 CAGCAGCAGAGCTTTCATCAT 21  
1 CAGCAGCAGAGCTTTCATCAT 21

GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Stolk, John A.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.484C5  
CURRENT APPLICATION NUMBER: US/09/825,294  
CURRENT FILING DATE: 2001-04-03  
NUMBER OF SEQ ID NOS: 215  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 396  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURES:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(396)  
OTHER INFORMATION: n = A,T,C or G  
US-09-825-294-15  
Query Match  
Best Local Similarity 100.0%; Score 21; DB 9; Length 396;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 CAGCAGCAGAGCTTTCATCAT 21  
79 CAGCAGCAGAGCTTTCATCAT 59  
RESULT 5  
US-09-970-966-15/c  
Sequence 15, Application US/09970966  
Patent No. US20020173638A1  
GENERAL INFORMATION:  
APPLICANT: Stolk, John A.  
APPLICANT: Molesch, David Alan  
APPLICANT: Fling, Steven P.  
APPLICANT: Xu, Jiangchun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.484C6  
CURRENT APPLICATION NUMBER: US/09/970,966  
CURRENT FILING DATE: 2001-10-02  
NUMBER OF SEQ ID NOS: 215  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 396  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURES:  
NAME/KEY: misc\_feature  
LOCATION: 333  
OTHER INFORMATION: n = A,T,C or G  
US-09-970-966-15  
Query Match  
Best Local Similarity 100.0%; Score 21; DB 10; Length 396;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 CAGCAGCAGAGCTTTCATCAT 21  
79 CAGCAGCAGAGCTTTCATCAT 59  
RESULT 6  
US-10-212-677-15/c  
Sequence 15, Application US/10212677  
Publication No. US20030129192A1  
GENERAL INFORMATION:  
APPLICANT: Cheneault, Ruth A.  
APPLICANT: Xu, Jiangchun

APPLICANT: Fanger, Gary R.  
 APPLICANT: Harlocker, Susan L.  
 APPLICANT: McNeill, Patricia D.  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
 FILE REFERENCE: 210121.484C7  
 CURRENT APPLICATION NUMBER: US/10/212,677  
 CURRENT FILING DATE: 2002-08-02  
 NUMBER OF SEQ ID NOS: 288  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 15  
 LENGTH: 396  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 333  
 OTHER INFORMATION: n = A,T,C or G  
 -10-212-677-15

Query Match 100.0%; Score 21; DB 15; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 2.3;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21  
 79 CAGCAGCAGAGCTTCATCAT 59

SULT 7  
 -09-918-995-32172/c  
 Sequence 32172, Application US/09918995  
 Publication No. US20030073623A1  
 GENERAL INFORMATION:  
 APPLICANT: Hyseq, Inc.  
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES  
 FILE REFERENCE: 20411-756  
 CURRENT APPLICATION NUMBER: US/09/918,995  
 CURRENT FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: US/09/235,076  
 PRIOR FILING DATE: 1999-01-20  
 NUMBER OF SEQ ID NOS: 38054  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 32172  
 LENGTH: 461  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1) -- (461)  
 OTHER INFORMATION: n = A,T,C or G  
 -09-918-995-32172

Query Match 100.0%; Score 21; DB 11; Length 461;  
 Best Local Similarity 100.0%; Pred. No. 2.3;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21  
 130 CAGCAGCAGAGCTTCATCAT 110

TIT 8  
 -09-918-995-2524/c  
 Sequence 2524, Application US/09918995  
 Publication No. US20030073623A1  
 GENERAL INFORMATION:  
 APPLICANT: Hyseq, Inc.  
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES  
 FILE REFERENCE: 20411-756  
 CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: US/09/235,076  
 PRIOR FILING DATE: 1999-01-20  
 NUMBER OF SEQ ID NOS: 38054  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 2524  
 LENGTH: 462  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1) -- (462)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-918-995-2524

Query Match 100.0%; Score 21; DB 11; Length 462;  
 Best Local Similarity 100.0%; Pred. No. 2.3;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTCATCAT 21  
 Db 115 CAGCAGCAGAGCTTCATCAT 95

RESULT 9  
 US-09-918-995-32177/c  
 Sequence 32177, Application US/09918995  
 Publication No. US20030073623A1  
 GENERAL INFORMATION:  
 APPLICANT: Hyseq, Inc.  
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES  
 FILE REFERENCE: 20411-756  
 CURRENT APPLICATION NUMBER: US/09/918,995  
 CURRENT FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: US/09/235,076  
 PRIOR FILING DATE: 1999-01-20  
 NUMBER OF SEQ ID NOS: 38054  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 32177  
 LENGTH: 465  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1) -- (465)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-918-995-32177

Query Match 100.0%; Score 21; DB 11; Length 465;  
 Best Local Similarity 100.0%; Pred. No. 2.3;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTCATCAT 21  
 Db 122 CAGCAGCAGAGCTTCATCAT 102

RESULT 10  
 US-09-918-995-12511/c  
 Sequence 12511, Application US/09918995  
 Publication No. US20030073623A1  
 GENERAL INFORMATION:  
 APPLICANT: Hyseq, Inc.  
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES  
 FILE REFERENCE: 20411-756  
 CURRENT APPLICATION NUMBER: US/09/918,995  
 CURRENT FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: US/09/235,076  
 PRIOR FILING DATE: 1999-01-20  
 NUMBER OF SEQ ID NOS: 38054  
 SOFTWARE: FastSeq for Windows Version 3.0

EQ ID NO 12511  
 LENGTH: 490  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: (1)...(490)  
 OTHER INFORMATION: n = A,T,C or G  
 09-918-995-12511

Query Match 100.0%; Score 21; DB 11; Length 490;  
 Best Local Similarity 100.0%; Pred. No. 2.3;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21  
 123 CAGCAGCAGAGCTTCATCAT 103

JLT 11  
 09-918-995-17455/C  
 Sequence 17455, Application US/09918995  
 Publication No. US20030073623A1  
 GENERAL INFORMATION:  
 APPLICANT: Hyseq, Inc.  
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 FROM VARIOUS CDNA LIBRARIES  
 FILER REFERENCE: 20411-756  
 CURRENT APPLICATION NUMBER: US/09/918, 995  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: US/09/235,076  
 PRIOR FILING DATE: 1999-01-20  
 NUMBER OF SEQ ID NOS: 38054  
 SOFTWARE: FastSeq for Windows Version 3.0  
 30 ID NO 17455  
 LENGTH: 491  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: (1)...(491)  
 OTHER INFORMATION: n = A,T,C or G  
 09-918-995-17455

Query Match 100.0%; Score 21; DB 11; Length 491;  
 Best Local Similarity 100.0%; Pred. No. 2.3;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21  
 134 CAGCAGCAGAGCTTCATCAT 114

JLT 12  
 09-918-995-31156/C  
 Sequence 31156, Application US/09918995  
 Publication No. US20030073623A1  
 GENERAL INFORMATION:  
 APPLICANT: Hyseq, Inc.  
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 FROM VARIOUS CDNA LIBRARIES  
 FILER REFERENCE: 20411-756  
 CURRENT APPLICATION NUMBER: US/09/918, 995  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: US/09/235,076  
 PRIOR FILING DATE: 1999-01-20  
 NUMBER OF SEQ ID NOS: 38054  
 SOFTWARE: FastSeq for Windows Version 3.0  
 30 ID NO 31156  
 LENGTH: 492  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:

NAME/KEY: misc.feature  
 LOCATION: (1)...(492)  
 OTHER INFORMATION: n = A,T,C or G  
 09-918-995-31156

Query Match 100.0%; Score 21; DB 11; Length 492;  
 Best Local Similarity 100.0%; Pred. No. 2.3;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21  
 Db 108 CAGCAGCAGAGCTTCATCAT 88

RESULT 13  
 US-09-833-381-910/C  
 Sequence 910, Application US/09833381  
 Patent No. US20020132090A1  
 GENERAL INFORMATION:  
 APPLICANT: Robison, Keith E.  
 TITLE OF INVENTION: NO. US20020132090A1 Nucleic Acid and Protein Homologs  
 FILER REFERENCE: 5800-119  
 CURRENT APPLICATION NUMBER: US/09/833,381  
 PRIOR FILING DATE: 2001-04-11  
 PRIOR APPLICATION NUMBER: 09/516,448  
 PRIOR FILING DATE: 2000-02-29  
 NUMBER OF SEQ ID NOS: 2050  
 SOFTWARE: FastSeq for Windows Version 3.0  
 30 ID NO 910  
 LENGTH: 532  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: (1)...(532)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-833-381-910

Query Match 100.0%; Score 21; DB 10; Length 532;  
 Best Local Similarity 100.0%; Pred. No. 2.4;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21  
 Db 93 CAGCAGCAGAGCTTCATCAT 73

RESULT 14  
 US-10-133-013-214/C  
 Sequence 214, Application US/10133013  
 Publication No. US20030166903A1  
 GENERAL INFORMATION:  
 APPLICANT: Astronomoff, Anna  
 APPLICANT: Bandman, Olga  
 APPLICANT: Cocks, Benjamin G.  
 TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE  
 FILER REFERENCE: PA-0049 US  
 CURRENT APPLICATION NUMBER: US/10/133,013  
 PRIOR FILING DATE: 2002-04-25  
 PRIOR APPLICATION NUMBER: 60/287,067  
 PRIOR FILING DATE: 2001-04-27  
 NUMBER OF SEQ ID NOS: 271  
 SOFTWARE: PERL Program  
 30 ID NO 214  
 LENGTH: 1451  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc.feature  
 OTHER INFORMATION: Incyte ID No. US20030166903A1 474437.17  
 NAME/KEY: unsure  
 LOCATION: 1407

OTHER INFORMATION: a, t, c, g, or other  
-10-133-013-214

Query Match 100.0%; Score 21; DB 12; Length 1451;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21  
366 CAGCAGCAGAGTCTTCATCAT 346

30LT 15  
-10-119-428-31/c  
Sequence 31, Application US/10119428  
Publication No. US20030165861A1

GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Xu, Chongjun  
APPLICANT: Wehrman, Tom  
APPLICANT: Ren, Feiyun  
APPLICANT: Ma, Yungqing  
APPLICANT: Zhou, Ping  
APPLICANT: Zhao, Qing A.  
APPLICANT: Yang, Yonshong  
APPLICANT: Drmanac, Radjole T.

TITLE OF INVENTION: No. US20030165861A1 Nucleic Acids and  
TITLE OF INVENTION: Polypeptides  
FILE REFERENCE: 789CIP2  
CURRENT APPLICATION NUMBER: US/10/119,428  
CURRENT FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 09/596,193  
PRIOR FILING DATE: 2000-06-17  
PRIOR APPLICATION NUMBER: 09/574,454  
PRIOR FILING DATE: 2000-05-19  
PRIOR APPLICATION NUMBER: 09/519,705  
PRIOR FILING DATE: 2000-03-07  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: pc\_FL\_genes Version 1.0  
SEQ ID NO 31  
LENGTH: 1614

TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (116)..(1465)  
10-119-428-31

Query Match 100.0%; Score 21; DB 12; Length 1614;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21  
136 CAGCAGCAGAGTCTTCATCAT 116

rch completed: November 8, 2003, 02:48:52  
time : 245 secs

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nucleic - nucleic search, using sw model

on: November 8, 2003, 00:46:13 ; Search time 70 Seconds  
(without alignments)  
132.415 Million cell updates/sec

le: US-09-944-326-4

fluence: 1 cagcagcagcgttcacatc 21

ring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

arched: 569978 segs, 220691566 residues

al number of hits satisfying chosen parameters: 1139956

num DB seq length: 0  
num DB seq length: 2000000000

it-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

abase :  
1: /cgn2\_6/ptodata/2/ina/5A.COMB.seg:\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seg:\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seg:\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seg:\*  
5: /cgn2\_6/ptodata/2/ina/PTCUS.COMB.seg:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seg:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	DB	ID	Description
1	21	100.0	181	2	US-08-485-657A-19	Sequence 19, Appl
2	21	100.0	181	4	US-09-366-380-19	Sequence 19, Appl
3	21	100.0	181	5	PCT-US95-02303-18	Sequence 18, Appl
4	21	100.0	195	2	US-08-485-657A-14	Sequence 14, Appl
5	21	100.0	195	4	US-09-366-380-14	Sequence 14, Appl
6	21	100.0	195	5	PCT-US95-02303-14	Sequence 14, Appl
7	21	100.0	1648	4	US-09-659-791A-3	Sequence 14, Appl
8	21	100.0	1651	4	US-09-659-791A-13	Sequence 13, Appl
9	21	100.0	7610	4	US-09-659-791A-12	Sequence 12, Appl
10	17.4	82.9	633	3	US-08-950-925-1	Sequence 1, Appl
11	17.4	82.9	633	4	US-09-565-286-1	Sequence 1, Appl
12	17.4	82.9	651	2	US-08-961-858-1	Sequence 1, Appl
13	17.4	82.9	651	2	US-08-961-858-1	Sequence 1, Appl
14	17.4	82.9	651	3	US-09-089-593-1	Sequence 3, Appl
15	17.4	82.9	651	3	US-09-089-593-3	Sequence 3, Appl
16	17.4	82.9	651	3	US-08-993-380-5	Sequence 3, Appl
17	17.4	82.9	744	4	US-09-366-819A-1	Sequence 5, Appl
18	17.4	82.9	795	4	US-09-366-819A-1	Sequence 5, Appl
19	17.4	82.9	1173	3	US-08-993-380-3	Sequence 3, Appl
20	16.8	80.0	330	2	US-08-980-060-9	Sequence 9, Appl
21	16.8	80.0	330	3	US-09-307-185-9	Sequence 9, Appl
22	16.8	80.0	334	4	US-09-227-357-90	Sequence 90, Appl
23	16.8	80.0	1806	3	US-08-980-060-1	Sequence 1, Appl
24	16.8	80.0	1806	3	US-09-307-185-1	Sequence 1, Appl
25	16.8	80.0	3459	2	US-08-980-060-3	Sequence 3, Appl
26	16.8	80.0	3459	2	US-09-307-185-3	Sequence 3, Appl
27	16.4	78.1	1051	3	US-09-008-697A-21	Sequence 21, Appl

28	16.2	77.1	32	4	US-09-410-935B-6	Sequence 6, Appl1
29	16.2	77.1	139	4	US-09-345-882-12	Sequence 12, Appl
30	16.2	77.1	279	4	US-09-313-294A-2815	Sequence 2815, Ap
31	16.2	77.1	283	4	US-09-313-294A-1242	Sequence 1242, Ap
32	16.2	77.1	336	4	US-09-657-452A-17	Sequence 17, Appl
33	16.2	77.1	471	4	US-09-996-243-393	Sequence 393, App
34	16.2	77.1	480	4	US-09-118-554-56	Sequence 56, App
35	16.2	77.1	480	4	US-09-118-627-56	Sequence 56, Appl
36	16.2	77.1	480	4	US-09-247-155-41	Sequence 56, Appl
37	16.2	77.1	550	3	US-08-998-416-148	Sequence 41, Appl
38	16.2	77.1	578	4	US-09-602-877A-95	Sequence 148, App
39	16.2	77.1	588	1	US-08-139-937-9	Sequence 95, Appl
40	16.2	77.1	688	5	PCT-US93-11310-9	Sequence 9, Appl1
41	16.2	77.1	975	6	US-09-134-001C-1512	Sequence 1512, Ap
42	16.2	77.1	977	6	US-09-134-001C-1512	Sequence 1, Appl1
43	16.2	77.1	1539	4	US-08-684-101-1	
44	16.2	77.1	1677	2	US-08-684-101-1	
45	16.2	77.1				

ALIGNMENTS

RESULT 1  
US-08-485-657A-19/c  
Sequence 19, Application US/08485657A  
Patent No. 5942389  
GENERAL INFORMATION:  
APPLICANT: Kirschling, Deborah J  
APPLICANT: Gudkov, Andrei  
TITLE OF INVENTION: Genes and Genetic Elements Associated  
TITLE OF INVENTION: with Sensitivity to Cisplatin  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSER: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive, 32nd Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,657A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5942389nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 93,354-N  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
TELEX:  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 181 base pairs  
TYPE: nucleic acid  
STRANDBESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: CDNA  
US-08-485-657A-19  
Query Match 100.0%; Score 21; DB 2; Length 181;  
Best local similarity 100.0%; Pred. No. 0.96;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 CAGCAGCAGGTTTCATCAT 21  
|||||

73 CAGCAGCAGAGCTTTCATCAT 53

LT 2

9-366-380-19/c  
Sequence 19, Application US/09366380  
Item No. 6541603

GENERAL INFORMATION:  
APPLICANT: Kirschling, Deborah J  
APPLICANT: Gudkov, Andrei

TITLE OF INVENTION: Genes and Genetic Elements Associated  
NUMBER OF SEQUENCES: 23  
TITLE OF INVENTION: with Sensitivity to Cisplatin

CORRESPONDENCE ADDRESS:

ADDRESSER: McDowell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive, 32nd Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/366,380

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/199,900

FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: No. 6541603nan, Kevin E  
REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 93,354-N  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002

TELEX:

INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:

LENGTH: 181 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
9-366-380-19

ery Match 100.0%; Score 21; DB 4; Length 181;  
Best Local Similarity 100.0%; Pred. No. 0.96;  
tches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTTCATCAT 21  
73 CAGCAGCAGAGCTTTCATCAT 53

LT 3

US95-02303-18/c  
Sequence 18, Application PC/TUS9502303

GENERAL INFORMATION:

TITLE OF INVENTION: Genes and Genetic Elements Associated  
NUMBER OF SEQUENCES: 25  
TITLE OF INVENTION: with Sensitivity to Cisplatin

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/02303  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 181 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
PCT-US95-02303-18

Query Match 100.0%; Score 21; DB 5; Length 181;  
Best Local Similarity 100.0%; Pred. No. 0.96;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTTCATCAT 21  
Db 73 CAGCAGCAGAGCTTTCATCAT 53

RESULT 4  
US-08-485-657A-14/c  
Sequence 14, Application US/08485657A  
Patent No. 5942389  
GENERAL INFORMATION:  
APPLICANT: Kirschling, Deborah J  
APPLICANT: Gudkov, Andrei

TITLE OF INVENTION: Genes and Genetic Elements Associated  
NUMBER OF SEQUENCES: 23  
TITLE OF INVENTION: with Sensitivity to Cisplatin

CORRESPONDENCE ADDRESS:  
ADDRESSER: McDowell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive, 32nd Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,657A

FILING DATE: 07-JUN-1995  
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:  
NAME: No. 5942389nan, Kevin E  
REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 93,354-N  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002

TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:  
LENGTH: 195 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-485-657A-14

Query Match 100.0%; Score 21; DB 2; Length 195;  
Best Local Similarity 100.0%; Pred. No. 0.97;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTTCATCAT 21  
Db 87 CAGCAGCAGAGCTTTCATCAT 67

RESULT 5

S-09-366-380-14/C

Sequence 14, Application US/09366380  
Patent No. 6541603

GENERAL INFORMATION:

APPLICANT: Kirschling, Deborah J

APPLICANT: Gudkov, Andrei

APPLICANT: Roninson, Igor B

TITLE OF INVENTION: Genes and Genetic Elements Associated

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSER: McDonnell Boehnen Hulbert &amp; Berghoff

STREET: 300 South Wacker Drive, 32nd Floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/366,380

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/199,900

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: NO. 6541603man, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 93,354-N

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-913-0001

TELEFAX: 312-913-0002

TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 195 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: CDNA

-09-366-380-14

Query Match 100.0%; Score 21; DB 4; Length 195;

Best Local Similarity 100.0%; Pred. No. 0.97;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21

87 CAGCAGCAGAGCTTCATCAT 67

SULT 6

T-US95-02303-14/C

Sequence 14, Application PC/TUS9502303

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Genes and Genetic Elements Associated

NUMBER OF SEQUENCES: 25

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/02303

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 195 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
PCT-US95-02303-14

Query Match

Best Local Similarity 100.0%; Score 21; DB 5; Length 195;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGCTTCATCAT 21

Db 87 CAGCAGCAGAGCTTCATCAT 67

RESULT 7

US-09-659-791A-3/C

Sequence 3, Application US/09659791A

Patent No. 6383808

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Susan M. Preier

TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION

FILE REFERENCE: RTS-0156

CURRENT APPLICATION NUMBER: US/09/659,791A

CURRENT FILING DATE: 2000-09-11

NUMBER OF SEQ ID NOS: 90

SEQ ID NO 3

LENGTH: 1648

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (53) ... (1402)

US-09-659-791A-3

Query Match 100.0%; Score 21; DB 4; Length 1648;

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGCTTCATCAT 21

Db 73 CAGCAGCAGAGCTTCATCAT 53

RESULT 8

US-09-659-791A-13/C

Sequence 13, Application US/09659791A

Patent No. 6383808

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Susan M. Preier

TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION

FILE REFERENCE: RTS-0156

CURRENT APPLICATION NUMBER: US/09/659,791A

CURRENT FILING DATE: 2000-09-11

NUMBER OF SEQ ID NOS: 90

SEQ ID NO 13

LENGTH: 1651

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (199) ... (1545)

US-09-659-791A-13

Query Match 100.0%; Score 21; DB 4; Length 1651;

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGCTTCATCAT 21

Db 216 CAGCAGCAGAGCTTCATCAT 196



JUL 9  
 09-659-791A-12/c  
 Sequence 12, Application US/09659791A  
 Patent No. 6133808  
 GENERAL INFORMATION:  
 APPLICANT: Brett P. Monia  
 APPLICANT: Susan M. Pfeiler  
 TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
 FILE REFERENCE: RTS-0156  
 CURRENT FILING DATE: 2000-09-11  
 CURRENT APPLICATION NUMBER: US/09/659,791A  
 NUMBER OF SEQ ID NOS: 90  
 SEQ ID NO 12  
 LENGTH: 7610  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 NAME/KEY: unsure  
 LOCATION: 5461  
 OTHER INFORMATION: unknown  
 NAME/KEY: unsure  
 LOCATION: 5462  
 OTHER INFORMATION: unknown  
 09-659-791A-12  
 Query Match 100.0%; Score 21; DB 4; Length 7610;  
 Best Local Similarity 100.0%; Pred. No. 1.5; 0; Indels 0; Gaps 0;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 CAGCAGCAGAGTCTTCATC 21  
 5558 CAGCAGCAGAGTCTTCATC 5538  
 JUL 10  
 08-950-925-1/c  
 Sequence 1, Application US/08950925  
 Patent No. 6072040  
 GENERAL INFORMATION:  
 APPLICANT: Dave, Kirti I.  
 APPLICANT: Botyanszki, Janos  
 APPLICANT: Sincar, Eva  
 TITLE OF INVENTION: Stabilized Conjugates of Uncomplexed  
 TITLE OF INVENTION: Subunits of Multimeric Proteins  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: MORRISON & FORSTER  
 STREET: 755 PAGE MILL ROAD  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304-1018  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/950,925  
 FILING DATE:  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Axford, Laurie A  
 REGISTRATION NUMBER: 35,053  
 REFERENCE/DOCKET NUMBER: 32260-20004.20  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-813-5600  
 TELEFAX: 650-494-0792

TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 633 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 FEATURE:  
 NAME/KEY: Coding Sequence  
 LOCATION: 1...630  
 OTHER INFORMATION:  
 US-08-950-925-1  
 Query Match 82.9%; Score 17.4; DB 3; Length 633;  
 Best Local Similarity 94.7%; Pred. No. 4.5;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CAGCAGCAGAGTCTTCATC 19  
 DB 162 CAGCAGCAGAGTCTTCAGC 144  
 RESULT 11  
 US-09-565-286-1/c  
 Sequence 1, Application US/09565286  
 Patent No. 6491923  
 GENERAL INFORMATION:  
 APPLICANT: Dave, Kirti I.  
 APPLICANT: Botyanszki, Janos  
 APPLICANT: Sincar, Eva  
 TITLE OF INVENTION: STABILIZED CONJUGATES OF UNCOMPLEXED  
 TITLE OF INVENTION: SUBUNITS OF MULTIMERIC PROTEINS  
 FILE REFERENCE: 35574-22004.10  
 CURRENT APPLICATION NUMBER: US/09/565,286  
 CURRENT FILING DATE: 2000-05-02  
 PRIOR APPLICATION NUMBER: 08/950,925  
 PRIOR FILING DATE: 1997-10-15  
 PRIOR APPLICATION NUMBER: 08/730,111  
 PRIOR FILING DATE: 1996-10-15  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 1  
 LENGTH: 633  
 TYPE: DNA  
 ORGANISM: homo sapien  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1)...(633)  
 US-09-565-286-1  
 Query Match 82.9%; Score 17.4; DB 4; Length 633;  
 Best Local Similarity 94.7%; Pred. No. 4.5;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CAGCAGCAGAGTCTTCATC 19  
 DB 162 CAGCAGCAGAGTCTTCAGC 144  
 RESULT 12  
 US-08-961-858-1/c  
 Sequence 1, Application US/08961858  
 Patent No. 5834210  
 GENERAL INFORMATION:  
 APPLICANT: Liu, Shigui  
 APPLICANT: Shi, Qimei  
 TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: Klauber & Jackson  
 STREET: 411 Hackensack Avenue, 4th Floor  
 CITY: Hackensack  
 STATE: New Jersey

## COUNTRY: USA

ZIP: 07601

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,858

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Bsq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1112-1-044 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 651 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

3-08-961-858-1

## Query Match

Best Local Similarity 82.9%; Score 17.4; DB 2; Length 651;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATC 19

180 CAGCAGCAGAGCTTCAC 162

## RESULT 13

1-08-961-858-3/c

Sequence 3, Application US/08961858

Patent No. 5834210

GENERAL INFORMATION:

APPLICANT: Liu, Shigu

TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber &amp; Jackson

STREET: 411 Hackensack Avenue, 4th Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,858

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Bsq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1112-1-044 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 651 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

DESCRIPTION: native form

HYPOTHETICAL: NO

US-08-961-858-3

## Query Match

Best Local Similarity 82.9%; Score 17.4; DB 2; Length 651;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATC 19

180 CAGCAGCAGAGCTTCAC 162

## RESULT 14

US-09-089-593-1/c

Sequence 1, Application US/09089593

Patent No. 6060278

GENERAL INFORMATION:

APPLICANT: Liu, Shigu

TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber &amp; Jackson

STREET: 411 Hackensack Avenue, 4th Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/089,593

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/961,858

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Bsq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1112-1-044 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 651 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

US-09-089-593-1

## Query Match

Best Local Similarity 82.9%; Score 17.4; DB 3; Length 651;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATC 19

180 CAGCAGCAGAGCTTCAC 162

SULT 15  
-09-089-593-3/c  
Sequence 3, Application US/09089593  
Patent No. 6060278  
GENERAL INFORMATION:

APPLICANT: Liu, Shigui  
APPLICANT: Shi, Qiwel  
TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:

ADDRESSER: Klauber & Jackson  
STREET: 411 Hackensack Avenue, 4th Floor  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/089,593  
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/961,858

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1112-1-044 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 651 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

DESCRIPTION: native form

HYPOTHETICAL: NO

-09-089-593-3

Query Match 82.9%; Score 17.4; DB 3; Length 651;

Local Similarity 94.7%; Pred. No. 45;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATC 19

|||||

180 CAGCAGCAGAGTCTTCAGC 162

Search completed: November 8, 2003, 01:50:57  
Time: 71 secs

GenCore version 5.1.6  
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nucleic - nucleic search, using sw model

on: November 8, 2003, 00:41:58 / Search time 256 Seconds  
(without alignments)  
221.438 Million cell updates/sec

le: US-09-944-326-4

fect score: 21

fluence: 1 cagcagcagcgtccatcat 21

ring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

arched: 2552756 seqs, 1349719017 residues

al number of hits satisfying chosen parameters: 5105512

imum DB seq length: 0

imum DB seq length: 2000000000

it-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

abase :  
N: Geneseg\_19Jun03:  
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22: /SIDS1/gcgdata/geneseg/geneseg-emb1/NA2001A.DAT:  
23: /SIDS1/gcgdata/geneseg/geneseg-emb1/NA2001B.DAT:  
24: /SIDS1/gcgdata/geneseg/geneseg-emb1/NA2002.DAT:  
25: /SIDS1/gcgdata/geneseg/geneseg-emb1/NA2003.DAT:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

ult No.	Score	Query Match	Length DB	ID	Description
1	21	100.0	21	AAA94226	Human testosterone
2	21	100.0	195	AAT00416	Genetic suppressor
3	21	100.0	275	AAC06940	Human secreted pro
4	21	100.0	395	AA94824	Human ovarian carc
5	21	100.0	396	AB703091	Human ovarian carc
6	21	100.0	396	ABL48774	Ovarian carcinoma
7	21	100.0	491	AAC03751	Human secreted pro
8	21	100.0	512	AAV89150	EST clone CGI. HO

C	9	21	100.0	572	20	AAZ42136
C	10	21	100.0	902	24	ABO56105
C	11	21	100.0	722	21	AAA43857
C	12	21	100.0	1024	25	AB283527
C	13	21	100.0	1568	22	AA544948
C	14	21	100.0	1589	24	AB78654
C	15	21	100.0	1648	24	ABN96656
C	16	21	100.0	1651	12	AAQ11503
C	17	21	100.0	1651	24	ABN96666
C	18	21	100.0	1678	22	AAH23086
C	19	21	100.0	1712	24	AB578651
C	20	21	100.0	7610	24	ABN96665
C	21	18.4	87.6	215561	24	ABN71527
C	22	17.8	84.8	50	20	AAZ4790
C	23	17.8	84.8	366	25	ABX35023
C	24	17.8	84.8	377	25	ABX38693
C	25	17.8	84.8	379	25	ABX41456
C	26	17.8	84.8	389	25	ABX48928
C	27	17.8	84.8	413	25	ABX37325
C	28	17.8	84.8	414	25	ABX37324
C	29	17.8	84.8	414	25	ABX45607
C	30	17.8	84.8	416	25	ABX43344
C	31	17.8	84.8	417	17	AAT64832
C	32	17.8	84.8	418	17	AAT64834
C	33	17.8	84.8	426	17	AAT64833
C	34	17.8	84.8	426	25	ABX40866
C	35	17.8	84.8	446	21	AAC42717
C	36	17.8	84.8	448	21	AAC10235
C	37	17.8	84.8	460	17	AAT64831
C	38	17.8	84.8	520	24	AA46602
C	39	17.8	84.8	552	23	ABL10237
C	40	17.8	84.8	960	21	AAC45936
C	41	17.8	84.8	963	21	AAC42693
C	42	17.8	84.8	1201	21	AAC45344
C	43	17.8	84.8	2304	22	AA545136
C	44	17.8	84.8	2445	22	ACC46350
C	45	17.8	84.8	3050	23	ABL10236

## ALIGNMENTS

RESULT 1  
AAA94226  
ID AAA94226 standard; DNA; 21 BP.  
XX  
AC AAA94226;  
XX  
DT 12-JAN-2001 (first entry)  
XX  
DB Human testosterone-repressed prostate message-2 antisense oligo #2.  
XX  
KW Human: testosterone-repressed prostate message-2; TRPM-2; clusterin;  
XX sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200049937-A2.  
XX  
PD 31-AUG-2000.  
XX  
FP 25-FEB-2000; 2000MO-US04875.  
XX  
PR 26-FEB-1999; 99US-0121726.  
XX  
PA (UTBR-) UNIV BRITISH COLUMBIA.  
XX Gleave M, Rennie PS, Miyake H, Nelson C;  
XX WPI; 2000-533132/48.  
XX  
PT Treating prostatic tumors and renal cancers by antisense inhibition of  
PT the testosterone-repressed prostate messenger-2 gene -  
Drosophila melanog

Claim 3; Page 36; 38pp; English.

The present sequence is an antisense oligonucleotide directed at the human testosterone-repressed prostate message-2 (TRPM-2), also known as clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to promote the regression of tumours, and oligonucleotides directed at human TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2 gene. These include prostate cancer, renal cell cancer and some breast cancer cells. In addition to this, they also increase the chemosensitivity of the cells, meaning that conventional chemotherapy is more effective.

Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21  
1 CAGCAGCAGAGTCTTCATCAT 21

LT 2

10416/C  
AAT00416 standard; cDNA; 195 BP.

AAT00416;

26-MAR-1996 (first entry)

Genetic suppressor element HL7.1.

Genetic suppressor element; GSB; platinum-based drug; cisplatin; chemotherapy; HL7.1; testosterone-repressed prostatic message-2; TRPM-2; ss.

Synthetic.

W09522612-A2.

24-AUG-1995.

22-FEB-1995; 95MO-US02303.

22-FEB-1994; 94US-0199900.

(UNIT) UNIV ILLINOIS FOUND.

Gudkov A, Kirschling DJ, Roninson IB;

WPI; 1995-302718/39.

Genetic suppressor elements which confer resistance to platinum-based drugs, eg. cisplatin, on cancer cells - useful for enhancement of chemotherapy, and for diagnosis of resistance to these drugs.

Claim 14; Fig 17; 75pp; English.

The sequences represented by AAT00405-T00418 are genetic suppressor elements (GSBs). This sequence represents GSB HL6.10. This sequence shows homology to the cDNA encoding testosterone-repressed prostatic message-2 (TRPM-2). These sequences were obtained from a cDNA library derived from the total cDNA of a cisplatin sensitive cell. Genetic suppressor elements confer resistance to platinum-based drugs (pds), such as cisplatin. These functional GSBs can then be used to create probes for the parent gene. The probes can then be used in a method of measuring the level of GSB gene expression. The GSBs can be used in methods of diagnosis of resistance to pds by measuring the level of expression of GSB genes. The GSBs are also used in methods to overcome resistance to pds in cancer cells. The GSBs (or fragments of them) can

be used to inhibit the function of genes associated with sensitivity to pds. For enhancement of chemotherapy, a GSB can be transferred (either alone or with another gene) on an expression vector into blood progenitor cells from a cancer patient. The cells are returned to the patient's circulation and allowed to repopulate the blood before aggressive chemotherapy is carried out (using higher cisplatin concentrations than normal), this will thereby avoid toxic side effects to the immune system as the blood cells will be GSB resistant.

Sequence 195 BP; 46 A; 45 C; 71 G; 33 T; 0 other;

Query Match 100.0%; Score 21; DB 16; Length 195;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21  
Db 87 CAGCAGCAGAGTCTTCATCAT 67

RESULT 3

AAC06940/C  
ID AAC06940 standard; cDNA; 275 BP.

AAC06940;

06-OCT-2000 (first entry)

Human secreted protein 5' EST, SEQ ID NO: 11015.

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.

Homo sapiens.

EP1033401-A2.

06-SEP-2000.

21-FEB-2000; 2000EP-0200610.

26-FEB-1999; 99US-0122487.

(GEST) GENSET.

Dumas Milne Edwards J, Duclert A, Giordano J;

WPI; 2000-500381/45.

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures - Claim 1; SEQ ID 11015; 71pp + CD-ROM; English.

The present sequence is one of a large number of 5' ESTs derived from cDNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.

Sequence 275 BP; 59 A; 88 C; 85 G; 43 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 275;

Best Local Similarity 100.0%; Pred. No. 5.4;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21  
|||||  
128 CAGCAGCAGAGTCTTCATCAT 108

3ULF 4  
794824/C  
AAP94824 standard; cDNA; 396 BP.

AAP94824;

23-MAY-2001 (first entry)

Human ovarian cancer associated coding sequence SEQ ID NO: 15.

Human, ovarian cancer; vaccine; gene therapy; carcinoma; ss.

Homo sapiens.

MO200118046-A2.

15-MAR-2001.

08-SEP-2000; 2000MO-US24827.

10-SEP-1999; 99US-0394374.

01-MAY-2000; 2000US-0561778.

15-AUG-2000; 2000US-0640173.

07-SEP-2000; 2000US-0656668.

(CORI-) CORIXA CORP.

Xu J, Stolk JA;

WPI; 2001-211395/21.

Isolated polypeptides associated with ovarian carcinomas, and the nucleic acids that encode them, useful for the prevention diagnosis and treatment of ovarian cancers.

Claim 18; Page 120; 1899p; English.

The present invention provides a number of coding sequences and proteins, the over-expression of which is associated with ovarian carcinoma/cancer. These can be used in the diagnosis, treatment and prevention of ovarian cancer, optionally by gene therapy or in the form of a vaccine. The present sequence is an example of one of these sequences.

Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 1 other;

very Match 100.0%; Score 21; DB 22; Length 396;

est Local Similarity 100.0%; Pred. No. 5.7;  
atches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21  
|||||  
79 CAGCAGCAGAGTCTTCATCAT 59

ULF 5

03091/C  
ABT03091 standard; cDNA; 396 BP.

ABT03091;

05-SEP-2002 (first entry)

Human ovarian carcinoma associated coding sequence SEQ ID NO: 15.

Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

KW cytosolic; gene; ss.

XX Homo sapiens.

OS WO200239885-A2.

XX 23-MAY-2002.

XX 13-NOV-2001; 2001WO-US45395.

XX 14-NOV-2000; 2000US-0713550.

XX 03-APR-2001; 2001US-0825294.

XX 02-OCT-2001; 2001US-0970966.

XX (CORI-) CORIXA CORP.

XX Xu J, Stolk JA, Algate PA, Fling SP, Moleen DA;

XX WPI; 2002-500186/53.

XX Novel ovarian cancer polypeptide and polynucleotide, useful for detecting the presence of ovarian cancer in a patient, and in pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

XX Example 1; Page 117; 197p; English.

XX The present invention provides human ovarian cancer associated proteins and coding sequences. The sequences can be used in the diagnosis and treatment of ovarian cancers. The present sequence is a coding sequence of the invention.

XX Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 1 other;

SO Query Match

Best Local Similarity 100.0%; Pred. No. 5.7; Length 396;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAGCAGCAGAGTCTTCATCAT 21  
|||||

Db 79 CAGCAGCAGAGTCTTCATCAT 59

RESULT 6  
ABT48774/C  
ID ABL48774 standard; cDNA; 396 BP.

XX ABL48774;

XX 18-JUN-2002 (first entry)

XX Ovarian carcinoma sequence isolate 23657.1.

XX Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;

XX ss.

XX Homo sapiens.

XX US2002004491-A1.

XX 10-JAN-2002.

XX 03-APR-2001; 2001US-0825294.

XX 10-SEP-1999; 99US-0394374.

XX 01-MAY-2000; 2000US-0561778.

XX 15-AUG-2000; 2000US-0640173.

XX 07-SEP-2000; 2000US-0656668.

XX 14-NOV-2000; 2000US-0713550.

XX (XUJ/) XU J.

XX (STOLK/) STOLK J A.

XX (ALGATE/) ALGATE P A.

(FLIN/) FLING S P.

Xu J, Scolk JA, Algate PA, Fling SP;

WPI; 2002-171027/22.

Ovarian tumour polypeptide and polynucleotide useful in diagnosis, prevention and/or treatment of cancer, especially ovarian cancer -

Example 1; Page 43; 131pp; English.

The invention relates to ovarian tumour polynucleotides and polypeptides that may be utilized in cancer therapy, for example in a vaccine or gene therapy. Polypeptides and polynucleotides of the invention are useful for detecting a cancer in a patient, for stimulating and/or expanding T-cells specific for a tumour protein, and for inhibiting the development of a cancer in a patient. They are also useful for stimulating an immune response in a patient, and for treating a cancer in a patient and for determining the presence of a cancer in a patient. The isolated polynucleotides of the invention are useful for their ability to selectively form duplex molecules with complementary stretches of the entire desired gene or gene fragments, and for designing and preparing ribozyme molecules for inhibiting expression of tumour polypeptides in tumour cells. Polypeptides and polynucleotides of the invention are also useful in recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. The sequences given in records ABL48760-ABL48956 represent polynucleotides encoding ovarian carcinoma proteins.

Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 1 other;

Query Match 100.0%; Score 21; DB 24; Length 396;  
Local Similarity 100.0%; Pred. No. 5.7;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21  
|||||  
79 CAGCAGCAGAGCTTCATCAT 59

LT 7  
3751/C  
AAC03751 standard; cDNA; 491 BP.

AAC03751;  
06-OCT-2000 (first entry)

Human secreted protein 5' EST, SEQ ID NO: 3749.

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.

Homo sapiens.

EP1033401-A2.

06-SEP-2000.

21-FEB-2000; 2000BP-0200610.

26-FEB-1999; 99US-0122487.

(GEST) GENSET.

Dumas Milne Edwards J, Duclert A, Giordano J;

WPI; 2000-500381/45.

P-PSDB; AAG03745.

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -

XX Claim 1; SEQ ID 3749; 71pp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from  
XX mRNAs encoding secreted proteins. An ORF has been identified within the  
CC mRNAs encoding secreted proteins. EST sequences usually correspond  
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs  
CC derived from 30 different tissues. EST sequences usually correspond  
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are  
CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not  
CC well suited for isolating cDNA sequences derived from the 5' ends of  
CC mRNAs and even in those cases where longer cDNA sequences have been  
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from  
CC mRNAs with intact 5' ends and can therefore be used to obtain full length  
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,  
CC gene therapy and chromosome mapping procedures. They are used to obtain  
CC upstream regulatory sequences and to design expression and secretion  
CC vectors.

XX Sequence 491 BP; 149 A; 114 C; 149 G; 78 T; 1 other;

Query Match 100.0%; Score 21; DB 21; Length 491;  
Best Local Similarity 100.0%; Pred. No. 5.9;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTCATCAT 21  
|||||  
Db 128 CAGCAGCAGAGCTTCATCAT 108

RESULT 8  
AAV89150/c  
ID AAV89150 standard; cDNA; 512 BP.

XX AAV89150;

DT 15-FEB-1999 (first entry)  
DE EST clone CG1.

KW Human; secreted protein; expressed sequence tag; EST; haematopoiesis;  
KW tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;  
KW receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;  
KW gene therapy; ss.

XX Homo sapiens.

PN MO9845436-A2.

XX 15-OCT-1998.

XX 10-APR-1998; 98MO-US06955.

XX 10-APR-1997; 97US-0838821.

XX (GENY) GENNETICS INST INC.

PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;  
PI Racie LA, Spaulding V, Treacy M;

XX WPI; 1999-070077/06.

PT New polynucleotides encoding human secreted proteins - derived from  
PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,  
PT ovary, pituitary, retina and colon cDNA libraries.

XX Claim 1; Page 126; 618pp; English.

XX The present sequence represents a human expressed sequence tag (EST).  
CC The polynucleotide, which is a secreted EST, and the encoded protein  
CC are predicted to have useful biological activities which would make  
CC them suitable for treating, preventing or ameliorating medical  
CC conditions in humans and animals, although no supporting data is  
CC given. Suggested activities include nutritional activity, immune

stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy.

Sequence 512 BP; 154 A; 114 C; 150 G; 94 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 512;  
Best Local Similarity 100.0%; Pred. No. 5.9;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21  
|||||  
55 CAGCAGCAGAGTCTTCATCAT 35

HLT 9  
42136/c  
AA242136 standard; cDNA; 572 BP.

AA242136;

31-JAN-2000 (first entry)

Human normal bladder tissue cDNA derived EST 15.

Human; bladder; treatment; EST; expressed sequence tag; cytostatic; cancer; gene therapy; ss.

Homo sapiens.

DE19818620-A1.

28-OCT-1999.

21-APR-1998; 98DE-1018620.

21-APR-1998; 98DE-1018620.

(META-) METAGEN GBS GENOMFORSCHUNG MBH.

Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

WPI; 1999-602416/52.

New polypeptides and their nucleic acids, useful for treatment of bladder tumour and identification of therapeutic agents

Claim 3; Page 158; 366pp; German.

This invention describes novel polypeptide fragment sequences (I) and their encoding nucleic acids (II) which are highly expressed in normal bladder tissue and have cytoskeletal activity. (II) are used for recombinant expression of (I) and to isolate complete genes. (I) are used to identify agents suitable for the treatment of bladder tumours, therapy vectors), or are used in a preparation for cancer treatment. (I) is also used for the generation of specific antibodies. (II) are identified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, and therefore reduces the number of failures because of ESTs from different libraries representing different parts of the same unknown gene. Distorting the estimated frequency of occurrence in a particular tissue. AA242132-242248 represent EST fragments derived from a human normal bladder tissue cDNA library which encode the protein fragments represented in AA60323-Y60591.

Sequence 572 BP; 161 A; 128 C; 186 G; 97 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 572;

Best Local Similarity 100.0%; Pred. No. 6;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21  
|||||  
Db 196 CAGCAGCAGAGTCTTCATCAT 176

RESULT 10  
ABQ56105/c  
ID ABQ56105 standard; cDNA; 704 BP.

XX ABQ56105;

AC 22-AUG-2002 (first entry)

DE Human ovarian antigen HSPSH41 cDNA, SEQ ID NO:1985.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;  
KW inflammatory condition; immune disorder; blood disorder;  
KW cardiovascular disorder; respiratory disorder; neurological disorder;  
KW gastrointestinal disorder; urinary system disorder; drug screening;  
KW gene therapy; chromosome mapping; forensic analysis;  
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
KW antiinflammatory; gynaecological; reproductive; gene; ss.

OS Homo sapiens.

FN WO200200677-A1.

XX 03-JAN-2002.

XX 07-JUN-2001; 2001WO-US18569.

XX 07-JUN-2000; 2000US-209467P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Birse CE, Rosen CA;

XX WPI; 2002-147878/19.

DR P-PSDB; ABP43028.

PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
PT useful in the prevention, treatment and diagnosis of cancer (e.g.  
PT ovarian cancer), immune disorders, cardiovascular disorders and  
PT neurological diseases

PS Claim 1; SEQ ID NO 1985; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-  
CC ABP41328) and to cDNAs encoding them (ABQ54131-ABQ56105), and also  
CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
CC to the sequences of the invention. The invention additionally relates to  
CC recombinant vectors and host cells comprising human ovarian antigen  
CC polynucleotides, antibodies against human ovarian antigens, and the use  
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
CC treating, prognosing or preventing various ovary and/or breast-related  
CC disorders. Such conditions include ovarian cancer and breast cancer, and  
CC metastatic tumours of ovarian or breast origin, reproductive system  
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine  
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
CC vaginitis), immune disorders (e.g., congenital and acquired  
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
CC respiratory disorders, neurological disorders, gastrointestinal disorders  
CC and urinary system disorders. Ovarian antigen polypeptides and  
CC polynucleotides may also be used in screening for compounds which



modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present invention represents cDNA encoding a human ovarian antigen of the

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published\\_pcr\\_sequences](http://wipo.int/pub/published_pcr_sequences).

Sequence 704 BP; 180 A; 197 C; 199 G; 121 T; 7 other;

Query Match 100.0%; Score 21; DB 24; Length 704;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21  
|||||  
149 CAGCAGCAGAGCTTCATCAT 129

LT 11

3857/c  
AAA43857 standard; cDNA; 922 BP.

AAA43857;

21-AUG-2000 (first entry)

Human secreted expressed sequence tag SEQ ID NO:432.

Human; mouse; chicken; rat; secreted expressed sequence tag; SEST; expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiaesthetic; vulnery; antiparkinsonian; antitumor; osteoprotective; neuroprotective; nootropic; antiparasitic; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vasculin; autoimmune diabetes; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour; infection; depression; psoriasis; ss.

Homo sapiens.

WO200021991-A1.

20-APR-2000.

15-OCT-1999; 99WO-US24206.

15-OCT-1998; 98US-010436.

(GENY) GENETICS INST INC.

Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C, Merberg D, Treacy M, Bowman MR;

WPI; 2000-317938/27.

Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (SESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -

Claim 1; Page 316; 803pp; English.

AAA43426 to AAA45925 represent specifically claimed secreted expressed sequence tags (SESTs), isolated from human, mouse, chicken and rat tissue sources. The SESTs can have a range of activities depending on

CC the tissues they were isolated from. The activities include:  
CC chemotactic; proliferative; immunomodulatory; haematopoietic;  
CC chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;  
CC cytostatic; antibacterial; antifungal; antiviral; antidiabetic;  
CC antitumour; vulnery; antitumor; osteoprotective; neuroprotective;  
CC nootropic; antiparkinsonian; antiparasitic; cerebroprotective;  
CC anticonvulsant; and antidepressant. The SESTs can be used for gene  
CC therapy and in vaccines. The SESTs are useful as probes for the  
CC identification and isolation of full-length cDNAs and genomic DNA  
CC molecules which correspond to the SESTs. Proteins encoded by the SESTs  
CC are useful in assays for determining biological activity and raising  
CC antibodies. They may be useful for treatment of autoimmune disorders  
CC (multiple sclerosis, insulin dependent diabetes), allergic conditions  
CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,  
CC osteoporosis, osteoarthritis, central nervous system disorders  
CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation  
CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's  
CC disease), tumours, bacterial, fungal or viral infections, depression and  
CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given  
CC in the exemplification of the present invention.

SO Sequence 922 BP; 243 A; 265 C; 244 G; 166 T; 4 other;

Query Match 100.0%; Score 21; DB 21; Length 922;  
Best Local Similarity 100.0%; Pred. No. 6.4;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTCATCAT 21  
|||||  
Db 52 CAGCAGCAGAGCTTCATCAT 32

RESULT 12

AB283527/c  
ID AB283527 standard; cDNA; 1024 BP.

XX AB283527;

DT 14-MAY-2003 (first entry)

XX Toxicologically relevant human nucleotide sequence #686.

XX Toxicologically relevant gene; toxicological response; gene; ss.

OS Homo sapiens.

XX WO2003016500-A2.

XX 27-FEB-2003.

PF 16-AUG-2002; 2002WO-US26514.

PR 16-AUG-2001; 2001US-313080P.

XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

PI Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schneider K;

PI Alen P;

DR WPI; 2003-268322/26.

PT Determining a toxicological response to an agent, useful for screening  
PT of drugs, comprises comparing the expression profile of one or more  
PT human toxic response genes to a reference gene expression profile  
PT indicative of toxicity -

PS Claim 1; Page 232; 455pp; English.

CC The present invention describes a method (M1) for determining a  
CC toxicological response to an agent, which comprises comparing the  
CC expression profile of one or more human toxic response genes to a  
CC reference gene expression profile indicative of toxicity, and so  
CC determining the presence of a toxic response to the agent. Also

described: (1) an array comprising one or more polynucleotides selected from the genes corresponding to the partial sequences given in AB282842 to AB284764, or their fragments of at least 20 nucleotides, or homologues; and (2) determining if a gene putatively identified to be a toxic response gene plays a role on toxic response pathways by determining the expression profile of the gene after exposure of cells or a human subject to a known toxic pharmaceutical or industrial agent, comprising: (a) exposing cells to an agent or isolating cells from a human subject who was exposed to an agent; (b) obtaining the test gene expression profile for a putatively identified toxic response gene after exposure to a known toxic pharmaceutical or industrial agent; and (c) comparing the test profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of that gene after exposure to other known toxic compounds. The methods are useful for predicting and determining toxicological responses on a cellular, organ or system level. The arrays comprising the human genes are useful for toxicological screening of drugs, pharmaceutical compounds and chemicals.

Sequence 1024 BP; 262 A; 299 C; 278 G; 185 T; 0 other;

Query Match 100.0%; Score 21; DB 25; Length 1024;  
Best Local Similarity 100.0%; Pred. No. 6.4;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21  
|||||  
68 CAGCAGCAGAGCTTCATCAT 48

SUPL 13  
S44948/c  
AAS44948 standard; cDNA; 1568 BP.

AAS44948;

18-DEC-2001 (first entry)

cDNA encoding novel human secretory protein, Seq ID No 29.

Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen; ss.

Homo sapiens.

MO200166689-A2.

13-SEP-2001.

05-MAR-2001; 2001MO-US04942.

07-MAR-2000; 2000US-0519705.  
19-MAY-2000; 2000US-0574454.  
17-JUN-2000; 2000US-0596193.  
14-JUL-2000; 2000US-0619847.  
19-SEP-2000; 2000US-0665363.  
20-OCT-2000; 2000US-0693267.

(HYSS-) HYSEQ INC.

Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P, Zhao QA, Yang Y, Dmanac RT, Zhang J, Chen R, Xue AJ, Wang J;  
WPI; 2001-589934/66.  
P-PSDB; AA028048.

PT Novel polypeptides and nucleic acids obtained from cDNA libraries  
PT prepared from various human tissues, for diagnosis and treatment of  
PT cancer, neurological, inflammatory, and autoimmune disorders -  
XX  
XX  
PS Claim 1; SEQ ID No 29; 107bp; English.

The invention relates to novel isolated human secreted polypeptides (I), and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodelling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis. In addition, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, CC reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or CC fungal infections, autoimmune disorders e.g. multiple sclerosis, CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic CC reactions and conditions, such as asthma or other respiratory problems. In addition, (I) affects biorhythms or circadian cycles of rhythms, CC fertility, metabolism, catabolism, anabolism, storage or elimination of CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides CC analgesic effects or other pain reducing effects, immunoglobulin like CC activity and can act as an antigen in a vaccine composition to raise an CC immune response. AAS44920-AAS45295 represent novel human secreted protein coding sequences of the invention.

XX Sequence 1568 BP; 386 A; 456 C; 434 G; 292 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 1568;  
Best Local Similarity 100.0%; Pred. No. 6.8;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CAGCAGCAGAGCTTCATCAT 21  
|||||  
Db 90 CAGCAGCAGAGCTTCATCAT 70

RESULT 14

AB278654/c

XX AB278654 standard; cDNA; 1589 BP.

XX 16-DEC-2002 (first entry)

DE Human cDNA encoding CGDD12, INCTB 7503618CB1.

XX Human; ss; gene; cell growth; differentiation; death; CGDD; cancer;  
KW cell proliferative disorder; arteriosclerosis; atherosclerosis;  
KW cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis;  
KW polycythaemia vera; primary thrombocytopenia; developmental disorder;  
KW renal tubular acidosis; anaemia; mental retardation; epilepsy; AIDS;  
KW neurological disorder; Alzheimer disease; Parkinson's disease; asthma;  
KW reproductive disorder; infertility; autoimmune disorder; gout; allergy;  
KW autoimmune thyroiditis; acquired immunodeficiency syndrome; uveitis;  
KW autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection;  
KW diabetes mellitus; glomerulonephritis; irritable bowel syndrome;  
KW multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis;  
KW rheumatoid arthritis.

Homo sapiens.

MO200272830-A2.

19-SEP-2002.

08-FEB-2002; 2002MO-US03715.

09-FEB-2001; 2001US-26811P.  
23-FEB-2001; 2001US-271175P.  
08-MAR-2001; 2001US-274503P.  
09-MAR-2001; 2001US-274552P.

(INCY-) INCYTE GENOMICS INC.

Yue H, Yao MG, Ison CH, Lu Y, Warren BA, Elliott VS, Baughn MR,  
Ding L, Xu Y, Gietzen KJ, Tang TY, Lal PG, Dugan BM, Burford N,  
Lu DAM, Richardson TW, Tran UK, Khare R, Walla NK;  
MPI: 2002-72356/78.  
P-PSDB; ABG97361.

New human proteins associated with cell growth, differentiation and death, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), cancer, atherosclerosis or hepatitis

Claim 5; Page 180-181; 181pp; English.

The invention relates to an isolated polypeptide comprising CGDD1-12 (cell growth, differentiation and death), a naturally occurring amino acid sequence at least 90% identical to CGDD, a biologically active fragment or an immunogenic fragment. Also included are the polynucleotides encoding CGDD1-12, a recombinant polynucleotide comprising a promoter sequence operably linked to the CGDD polynucleotides, a cell transformed with the recombinant polynucleotide, a transgenic organism comprising the recombinant polynucleotide, anti-CGDD antibody, screening for compounds which bind to/modulate or are anti/agonists of CGDD or alter the expression of CGDD polynucleotides and a CGDD polynucleotide microarray.

The polypeptides, polynucleotides, agonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of CGDD, particularly cell proliferative (e.g. atherosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary thrombocytopaenia or cancer), developmental disorders (e.g. renal tubular acidosis, anaemia or mental retardation), neurological disorders (e.g. Alzheimer disease, Parkinson's disease or epilepsy), reproductive disorders (e.g. infertility or a disruption in the menstrual cycle), or autoimmune/inflammatory disorders (e.g. AIDS, (acquired immunodeficiency syndrome) allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus, glomerulonephritis, gout, irritable bowel syndrome, multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, rheumatoid arthritis, uveitis, or viral, bacterial, fungal, parasitic, protozoal or helminthic infections. They are also useful in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of proteins associated with CGDD. The present sequence encodes a CGDD protein.

Sequence 1589 BP; 407 A; 421 C; 466 G; 295 T; 0 other;

Query Match 100.0%; Score 21; DB 24; Length 1589;  
Best Local Similarity 100.0%; Pred. No. 6.8;  
atches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;1 CAGCAGCAGAGCTTCATCAT 21  
|||||  
98 CAGCAGCAGAGCTTCATCAT 78

UL: 15

ABN99656/c  
ID ABN99656 standard; DNA; 1648 BP.

XX AC ABN99656;

XX DT 16-AUG-2002 (first entry)

XX DE Human clusterin gene sequence 1.

XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
XX KW hypercholesterolemia; cardiovascular disorder; dg;  
XX KW hyperproliferative disorder; hyperlipidemic disorder.

XX OS Homo sapiens.

XX PN WO200222635-A1.

XX PD 21-MAR-2002.

XX PF 10-SEP-2001; 2001MO-US28235.

XX PR 11-SEP-2000; 2000US-0659791.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Freier SM;

XX DR MPI: 2002-404805/43.

XX P-PSDB; AAO15039.

PT PT Clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder

XX PS Example 13; Page 89-92; 125pp; English.

CC The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a human clusterin gene sequence.

XX SQ Sequence 1648 BP; 408 A; 488 C; 440 G; 312 T; 0 other;

Query Match 100.0%; Score 21; DB 24; Length 1648;  
Best Local Similarity 100.0%; Pred. No. 6.9;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 CAGCAGCAGAGCTTCATCAT 21  
|||||  
DB 73 CAGCAGCAGAGCTTCATCAT 53Search completed: November 8, 2003, 00:51:22  
Job time : 258 secs

GenCore version 5.1.6  
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nucleic - nucleic search, using sw model

on: November 8, 2003, 00:45:43 ; Search time 1410 Seconds  
(without alignments)  
609.292 Million cell updates/sec

le: US-09-944-326-4

effect score: 21

fluence: 1 cagcagcagcgttcacatcat 21

oring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

urched: 2888711 seqs, 2045481386 residues

al number of hits satisfying chosen parameters: 5777422

Hum DB seq length: 0  
Hum DB seq length: 2000000000

ic-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

GenBml: 1: gb\_ba: 2: gb\_hcg: 3: gb\_in: 4: gb\_om: 5: gb\_ov: 6: gb\_pat: 7: gb\_ph: 8: gb\_pl: 9: gb\_pr: 10: gb\_ro: 11: gb\_scs: 12: gb\_sy: 13: gb\_un: 14: gb\_vl: 15: gb\_wa: 16: gb\_fun: 17: gb\_hum: 18: gb\_in: 19: gb\_mu: 20: gb\_om: 21: gb\_or: 22: gb\_ov: 23: gb\_pat: 24: gb\_ph: 25: gb\_pl: 26: gb\_pr: 27: gb\_ro: 28: gb\_scs: 29: gb\_sy: 30: gb\_un: 31: gb\_vl: 32: gb\_wa: 33: gb\_fun: 34: gb\_hum: 35: gb\_in: 36: gb\_mu: 37: gb\_om: 38: gb\_or: 39: gb\_ov: 40: gb\_pat: 41: gb\_ph: 42: gb\_pl: 43: gb\_pr: 44: gb\_ro: 45: gb\_scs: 46: gb\_sy: 47: gb\_un: 48: gb\_vl: 49: gb\_wa: 50: gb\_fun: 51: gb\_hum: 52: gb\_in: 53: gb\_mu: 54: gb\_om: 55: gb\_or: 56: gb\_ov: 57: gb\_pat: 58: gb\_ph: 59: gb\_pl: 60: gb\_pr: 61: gb\_ro: 62: gb\_scs: 63: gb\_sy: 64: gb\_un: 65: gb\_vl: 66: gb\_wa: 67: gb\_fun: 68: gb\_hum: 69: gb\_in: 70: gb\_mu: 71: gb\_om: 72: gb\_or: 73: gb\_ov: 74: gb\_pat: 75: gb\_ph: 76: gb\_pl: 77: gb\_pr: 78: gb\_ro: 79: gb\_scs: 80: gb\_sy: 81: gb\_un: 82: gb\_vl: 83: gb\_wa: 84: gb\_fun: 85: gb\_hum: 86: gb\_in: 87: gb\_mu: 88: gb\_om: 89: gb\_or: 90: gb\_ov: 91: gb\_pat: 92: gb\_ph: 93: gb\_pl: 94: gb\_pr: 95: gb\_ro: 96: gb\_scs: 97: gb\_sy: 98: gb\_un: 99: gb\_vl: 100: gb\_wa: 101: gb\_fun: 102: gb\_hum: 103: gb\_in: 104: gb\_mu: 105: gb\_om: 106: gb\_or: 107: gb\_ov: 108: gb\_pat: 109: gb\_ph: 110: gb\_pl: 111: gb\_pr: 112: gb\_ro: 113: gb\_scs: 114: gb\_sy: 115: gb\_un: 116: gb\_vl: 117: gb\_wa: 118: gb\_fun: 119: gb\_hum: 120: gb\_in: 121: gb\_mu: 122: gb\_om: 123: gb\_or: 124: gb\_ov: 125: gb\_pat: 126: gb\_ph: 127: gb\_pl: 128: gb\_pr: 129: gb\_ro: 130: gb\_scs: 131: gb\_sy: 132: gb\_un: 133: gb\_vl: 134: gb\_wa: 135: gb\_fun: 136: gb\_hum: 137: gb\_in: 138: gb\_mu: 139: gb\_om: 140: gb\_or: 141: gb\_ov: 142: gb\_pat: 143: gb\_ph: 144: gb\_pl: 145: gb\_pr: 146: gb\_ro: 147: gb\_scs: 148: gb\_sy: 149: gb\_un: 150: gb\_vl: 151: gb\_wa: 152: gb\_fun: 153: gb\_hum: 154: gb\_in: 155: gb\_mu: 156: gb\_om: 157: gb\_or: 158: gb\_ov: 159: gb\_pat: 160: gb\_ph: 161: gb\_pl: 162: gb\_pr: 163: gb\_ro: 164: gb\_scs: 165: gb\_sy: 166: gb\_un: 167: gb\_vl: 168: gb\_wa: 169: gb\_fun: 170: gb\_hum: 171: gb\_in: 172: gb\_mu: 173: gb\_om: 174: gb\_or: 175: gb\_ov: 176: gb\_pat: 177: gb\_ph: 178: gb\_pl: 179: gb\_pr: 180: gb\_ro: 181: gb\_scs: 182: gb\_sy: 183: gb\_un: 184: gb\_vl: 185: gb\_wa: 186: gb\_fun: 187: gb\_hum: 188: gb\_in: 189: gb\_mu: 190: gb\_om: 191: gb\_or: 192: gb\_ov: 193: gb\_pat: 194: gb\_ph: 195: gb\_pl: 196: gb\_pr: 197: gb\_ro: 198: gb\_scs: 199: gb\_sy: 200: gb\_un: 201: gb\_vl: 202: gb\_wa: 203: gb\_fun: 204: gb\_hum: 205: gb\_in: 206: gb\_mu: 207: gb\_om: 208: gb\_or: 209: gb\_ov: 210: gb\_pat: 211: gb\_ph: 212: gb\_pl: 213: gb\_pr: 214: gb\_ro: 215: gb\_scs: 216: gb\_sy: 217: gb\_un: 218: gb\_vl: 219: gb\_wa: 220: gb\_fun: 221: gb\_hum: 222: gb\_in: 223: gb\_mu: 224: gb\_om: 225: gb\_or: 226: gb\_ov: 227: gb\_pat: 228: gb\_ph: 229: gb\_pl: 230: gb\_pr: 231: gb\_ro: 232: gb\_scs: 233: gb\_sy: 234: 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 1 CAGCAGCAGAGCTTCATCAT 21  
 73 CAGCAGCAGAGCTTCATCAT 53  
 12784/c AR302784 195 bp mRNA linear PAT 12-JUN-2003  
 NITON Sequence 14 from patent US 6541603.  
 SSION AR302784  
 ION AR302784.1 GI:31691271  
 ORDS  
 CR  
 GANISM  
 RENCE 1 (bases 1 to 195)  
 THORS Kirschling,D.J., Gudkov,A. and Robinson,I.B.  
 TL Gene and genetic elements associated with sensitivity to  
 URMAL Platinum-based drugs  
 source Location/Qualifiers  
 1.195  
 : COUNT 46 a 45 c 71 g 33 t  
 IN  
 Query Match 100.0%; Score 21; DB 6; Length 195;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 CAGCAGCAGAGCTTCATCAT 21  
 87 CAGCAGCAGAGCTTCATCAT 67  
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 0685/c BD030685 275 bp DNA linear PAT 27-AUG-2002  
 NITON Sequence tag and encoded human protein.  
 SSION BD030685  
 ION BD030685.1 GI:22572427  
 ORDS JP 2001269182-A/6931.  
 CR Homo sapiens (human)  
 GANISM Homo sapiens  
 RENCE 1 (bases 1 to 275)  
 THORS Edwards,J.B.D.M., Duclatir,B. and Jordan,J.Y.  
 TL Sequence tag and encoded human protein  
 URMAL Patent: JP 2001269182-A 6931 02-OCT-2001;  
 GENSET  
 OS Homo sapiens (human)  
 PN JP 2001269182-A/6931  
 PD 02-OCT-2001  
 PF 24-FEB-2000 JP 2000118773  
 PR 26-FEB-1999 US 60/122487  
 PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLATIR, JEAN YVES  
 PI JORDAN  
 PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC  
 C12N5/10,  
 PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC  
 G06F15/40  
 CC

FH Key Location/Qualifiers  
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 /db\_xref="taxon:9606"  
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 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 CAGCAGCAGAGCTTCATCAT 21  
 128 CAGCAGCAGAGCTTCATCAT 108  
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 RESULT 4  
 LOCUS AX093197 396 bp DNA linear PAT 30-MAR-2001  
 DEFINITION Sequence 15 from Patent WO0118046.  
 ACCESSION AX093197  
 VERSION AX093197.1 GI:13509646  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RERENCE Xu,J. and Stolk,J.A.  
 AUTHORS Ovarian tumor sequences and methods of use therefor  
 TITLE Patent: WO 0118046-A 15 15-MAR-2001;  
 JOURNAL CORIXA CORPORATION (US)  
 FEATURES  
 source 1.396  
 /organism="Homo sapiens"  
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 1 CAGCAGCAGAGCTTCATCAT 21  
 79 CAGCAGCAGAGCTTCATCAT 59  
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 RESULT 5  
 LOCUS BD117323 482 bp DNA linear PAT 18-SEP-2002  
 DEFINITION EST and encoded human protein.  
 ACCESSION BD117323  
 VERSION BD117323.1 GI:2212227  
 KEYWORDS JP 2002010789-A/9400.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RERENCE Edwards,J.B.D.M., Jobert,S. and Giordano,J.B.  
 AUTHORS EST and encoded human protein  
 TITLE Patent: JP 2002010789-A 9400 15-JAN-2002;  
 JOURNAL GENSET CORP  
 OS Homo sapiens (human)  
 PN JP 2002010789-A/9400  
 PD 15-JAN-2002  
 PF 07-AUG-2000 JP 2000280989  
 COMMENT

PR 05-AUG-1999 US 60/147499  
PI JEAN BAPTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN-EVE  
GIORDANO  
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC  
C12N1/21,  
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC  
C12N15/00  
CC EST and encoded human protein  
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1 CAGCAGCAGAGCTTCATCAT 21  
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96 CAGCAGCAGAGCTTCATCAT 76

SUBMIT 6  
027496/c  
CTBS BD027496 491 bp DNA linear PAT 27-AUG-2002  
DEFINITION Sequence tag and encoded human protein.  
REVISION BD027496.1 GI:22569238  
TWOARDS JP 2001269182-A/3742.  
TWOARDS Homo sapiens (human)  
TWOARDS Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 491)  
AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.  
TITLE Sequence tag and encoded human protein  
JOURNAL Patent: JP 2001269182-A 3742 02-OCT-2001;  
GENSET

MMENT OS Homo sapiens (human)  
PN JP 2001269182-A/3742  
PD 02-OCT-2001  
PP 24-FEB-2000 JP 2000118773  
PR 26-FEB-1999 US 60/122487  
PI JEAN BAPTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES  
PI JORDAN  
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC  
C12N5/10,  
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC  
G06F15/40  
CC score 6.3  
FH Key Location/Qualifiers  
FT CDS 108..455  
FT 819 peptide 108..161.  
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38 COUNT 149 a 114 c 149 g 78 t 1 others  
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Best Local Similarity 100.0%; Pred. No. 31;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21

DB 128 CAGCAGCAGAGCTTCATCAT 108  
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RESULT 7  
BD071299/c  
LOCUS  
DEFINITION Secreted expressed sequence tags (ESTs).  
ACCESSION BD071299.1 GI:22616902  
VERSION BD071299.1  
KEYWORDS JP 2001519667-A/109.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 512)  
AUTHORS Jacobs, K., McCoy, J.M., Lavallie, E.R., Racie, L.A., Merberg, D.,  
Treacy, M., Spaulding, V. and Agostino, M.J.  
TITLE Secreted expressed sequence tags (ESTs)  
JOURNAL Patent: JP 2001519667-A 109 23-OCT-2001;  
COMMENT GENETICS INSTITUTE INC  
OS Unidentified  
PN JP 2001519667-A/109  
PD 23-OCT-2001  
PP 10-APR-1998 JP 1998543069  
PR 10-APR-1997 US 08/838821  
PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI  
DAVID MERBERG,  
PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC  
C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC Strandedness:  
Double;  
CC Topology: Linear;  
CC Secreted expressed sequence tags (ESTs)  
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FT source 1. 512  
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1 CAGCAGCAGAGCTTCATCAT 21  
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55 CAGCAGCAGAGCTTCATCAT 35

RESULT 8  
AK093399/c  
LOCUS  
DEFINITION Homo sapiens cDNA FLJ36080 f1s, clone TEST1019872, highly similar  
to CLUSTERIN PRECURSOR.  
ACCESSION AK093399  
VERSION AK093399.1 GI:21752259  
KEYWORDS oligo capping, f1s (full insert sequence).  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1546)  
AUTHORS Nishi, T., Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H.,  
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,  
Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,  
Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,  
Kikuchi, H., Kanda, K., Wagatsuna, M., Murakawa, K., Kanehori, K.,  
Takahashi, Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y.,  
Sugano, S., Nagahari, K., Maeno, Y., Negai, K. and Isegai, T.  
TITLE NEBO human cDNA sequencing project

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1546)  
AUTHORS Isogai, T. and Yamamoto, J.  
TITLES Direct Submission  
JOURNAL Submitted (04-JUL-2002) Takao Isogai, Fij Project (HRI Team); 2-6-7  
Kazusa-Kamata, K. Katsuzaki, Chiba 292-0812, Japan  
(E-mail: genomics@rii.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
MEDLINE MEDO human cDNA sequencing project supported by Ministry of  
Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
Research Association for Biotechnology (RAB); cDNA library  
construction: Helix Research Institute (HRI) (supported by Japan  
Key Technology Center etc.); 5'-6-3'-end one pass sequencing: RAB,  
HRI, and Biotechnology Center, National Institute of Technology and  
Evaluation; clone selection for full insert sequencing: HRI and  
RAB; annotation: HRI and RAB.  
LOCATION/Qualifiers  
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1 CAGCAGCAGAGTTCATCAT 21  
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99 CAGCAGCAGAGTTCATCAT 79  
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00212/c  
AX600212 1589 bp DNA linear PAT 14-FEB-2003  
TINTION Sequence 24 from Patent WO02072830.  
SSION AX600212  
SION AX600212.1 GI:28400254  
WORDS  
RCE Homo sapiens (human)  
RGNISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
AUTHORS Yue, H., Yao, M.G., Ison, C.H., Lu, Y., Warren, B.A., Elliott, V.S.,  
Baughn, M.R., Ding, L., Xu, Y., Gietzen, K.J., Tang, T.Y., Lal, P.G.,  
Duggan, B.M., Burford, N., Lu, D.A., Richardson, T.W., Tran, U.K.,  
Khare, R. and Wallis, N.K.  
TITLES Proteins associated with cell growth, differentiation, and death  
JOURNAL Patent: WO 02072830-A 24 19-SEP-2002;  
Incyte Genomics, Inc. (US)  
LOCATION/Qualifiers  
TUES source  
1. .1589  
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/db\_xref="taxon:9606"  
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GIN 407 a 421 c 466 g 295 t  
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Best Local Similarity 100.0%; Pred. No. 29;  
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1 CAGCAGCAGAGTTCATCAT 21  
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98 CAGCAGCAGAGTTCATCAT 78  
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RESULT 10  
LOCUS AR208704 1648 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 3 from patent US 6383808.  
ACCESSION AR208704  
VERSION AR208704.1 GI:21509928  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1648)  
AUTHORS Mont, B.P. and Freiler, S.M.  
TITLES Antisense inhibition of clusterin expression  
JOURNAL Patent: US 6383808-A 3 07-MAY-2002;  
LOCATION/Qualifiers  
source  
1. .1648  
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73 CAGCAGCAGAGTTCATCAT 53  
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Db  
1 CAGCAGCAGAGTTCATCAT 21  
|||||  
73 CAGCAGCAGAGTTCATCAT 53  
|||||  
RESULT 11  
LOCUS HUMTRPM2A 1648 bp mRNA linear PRI 23-AUG-1996  
DEFINITION Human TRPM-2 mRNA, complete cds.  
ACCESSION M64722  
VERSION M64722.1 GI:339972  
KEYWORDS TRPM-2 protein.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
AUTHORS Wong, P., Pineault, J., Lakin, J., Taillefer, D., Leger, J., Wang, C.  
and Tenniswood, M.  
TITLES Genomic organization and expression of the rat TRPM-2 (clusterin)  
JOURNAL J. Biol. Chem. 268 (7), 5021-5031 (1993)  
MEDLINE 9318693  
PUBMED 7680346  
REFERENCE 2 (bases 1 to 1648)  
AUTHORS Wong, P., Taillefer, D., Lakin, J., Pineault, J., Chader, G. and  
Tenniswood, M.  
TITLES Molecular characterization of human TRPM-2/clusterin, a gene  
associated with sperm maturation, apoptosis and neurodegeneration  
JOURNAL Eur. J. Biochem. 221 (3), 917-925 (1994)  
MEDLINE 94237156  
PUBMED 8181474  
COMMENT Original  
FEATURES  
source  
location text: Human cDNA to mRNA.  
location/Qualifiers  
1. .1648  
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53. .1402  
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1 CAGCAGCAGAGCTTCATCAT 21  
73 CAGCAGCAGAGCTTCATCAT 53

1651 bp DNA linear PAT 26-JUL-1994  
blood plasma component having a biological activity of inhibiting  
cytolysis mediated by a cytolytic protein.

1651 bp DNA linear PAT 26-JUL-1994  
blood plasma component having a biological activity of inhibiting  
cytolysis mediated by a cytolytic protein.

1651 bp DNA linear PAT 26-JUL-1994  
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blood plasma component having a biological activity of inhibiting  
cytolysis mediated by a cytolytic protein.

1651 bp DNA linear PAT 26-JUL-1994  
blood plasma component having a biological activity of inhibiting  
cytolysis mediated by a cytolytic protein.

VERSION AR208714.1 GI:21509941  
KEYWORDS Unknown  
SOURCE Unknown  
ORGANISM Unknown  
REFERENCE 1 (bases 1 to 1651)  
AUTHORS Monia,B.P. and Freiler,S.M.  
TITLE Antisense inhibition of clusterin expression  
JOURNAL Patent: US 6383808-A 13 07-MAY-2002;  
FEATURES location/Qualifiers  
source 1..1651  
/organism="unknown"  
BASE COUNT 405 a 481 c 447 g 318 t  
ORIGIN

Query Match  
Best Local Similarity 100.0%; Score 21; DB 6; Length 1651;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21  
216 CAGCAGCAGAGCTTCATCAT 196

1651 bp mRNA linear PRI 27-APR-1993  
human complement cytolysis inhibitor (CLI) mRNA, complete cds.

1651 bp mRNA linear PRI 27-APR-1993  
human complement cytolysis inhibitor (CLI) mRNA, complete cds.

1651 bp mRNA linear PRI 27-APR-1993  
human complement cytolysis inhibitor (CLI) mRNA, complete cds.

1651 bp mRNA linear PRI 27-APR-1993  
human complement cytolysis inhibitor (CLI) mRNA, complete cds.

1651 bp mRNA linear PRI 27-APR-1993  
human complement cytolysis inhibitor (CLI) mRNA, complete cds.

1651 bp mRNA linear PRI 27-APR-1993  
human complement cytolysis inhibitor (CLI) mRNA, complete cds.

1651 bp mRNA linear PRI 27-APR-1993  
human complement cytolysis inhibitor (CLI) mRNA, complete cds.

1651 bp mRNA linear PRI 27-APR-1993  
human complement cytolysis inhibitor (CLI) mRNA, complete cds.

1651 bp mRNA linear PRI 27-APR-1993  
human complement cytolysis inhibitor (CLI) mRNA, complete cds.

1651 bp mRNA linear PRI 27-APR-1993  
human complement cytolysis inhibitor (CLI) mRNA, complete cds.

1651 bp mRNA linear PRI 27-APR-1993  
human complement cytolysis inhibitor (CLI) mRNA, complete cds.

1651 bp mRNA linear PRI 27-APR-1993  
human complement cytolysis inhibitor (CLI) mRNA, complete cds.



! COUNT 405 a 481 c 447 g 318 t  
 ! IN Unreported.  
 very Match 100.0%; Score 21; DB 9; Length 1651;  
 !st Local Similarity 100.0%; Pred. No. 29;  
 itches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21  
 216 CAGCAGCAGAGTCTTCATCAT 196

LT 15 1658 bp mRNA linear PRI 17-Apr-2003  
 9588/c Homo sapiens clusterin (complement lyse inhibitor, SP-40, 40,  
 NITON sulfated glycoprotein 2, testosterone-repressed prostate message 2,  
 apolipoprotein J), mRNA (cdna clone MGC:24903 IMAGE:4915444),  
 complete cds.  
 BC019588  
 BC019588 GI:18043614  
 MGC.

ION Homo sapiens (human)  
 ORDS  
 CR  
 GANISM

RENCE  
 THORS  
 1 (bases 1 to 1658)  
 Strausberg, R.L., Pelting, B.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
 Diatchenko, L., Marusik, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Stappleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
 Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,  
 Carninci, P., Prange, C., Raha, S.S., Loggellano, N.A., Peters, G.J.,  
 Abramson, R.D., Mulvihy, S.J., Bosak, S.A., McEwan, P.J.,  
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huiyk, S.W.,  
 Villalón, D.R., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,  
 Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,  
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
 Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,  
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.E.,  
 Schnerker, A., Schein, J.B., Jones, S.J., and Marra, M.A.

TLR  
 URAL  
 DLIN  
 URMED  
 RENCE  
 THORS  
 TLR  
 URAL

Submitted (19-DEC-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

NIH-MGC Project URL: http://mgc.nci.nih.gov  
 Contact: MGC help desk  
 Email: cgabs-remail.nih.gov

Tissue Procurement: David N. Louis, M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)  
 DNA Sequencing by: Baylor College of Medicine Human Genome  
 Sequencing Center  
 Center code: BCM-HGSC  
 Web site: http://www.hgsc.bcm.tmc.edu/cdna/  
 Contact: amg@bcm.tmc.edu  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Loulsged, H.,  
 Kowls, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,  
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/ILNLI at: http://image.llnl.gov  
 Series: IRAC Plate: 29 Row: m Column: 21  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 4502904.  
 Location/Qualifiers

FEATURES  
 source  
 1.1658  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="MGC:24903 IMAGE:4915444"  
 /tissue\_type="Brain, anaplastic oligodendroglioma with"  
 /lab\_host="DH10B"  
 /note="Vector: pCMV-SPORT6"  
 1.1658  
 /gene="CLU"  
 /note="Synonyms: APOJ, CLI, SP-40, SGP-2, SGP2, TRPM-2,  
 TRPM2"  
 /db\_xref="LOCUSID:1191"  
 /db\_xref="MIM:185430"  
 49.1398  
 /codon\_start=1  
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 sulfated glycoprotein 2, testosterone-repressed prostate  
 message 2, apolipoprotein J)"  
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 /db\_xref="LOCUSID:1191"  
 /translation="MKTLLEPVGLLTVESGVLAGDQTVSDNBLQEMSNQSKYVVK  
 EIONAVNGVQKIKLTKTERKTLISLBAKKKKEDALNBTRESFKLELPVC  
 NETMALMECKPCIKOKMRYARVCRSGSLVGRLEEFINQSSPPYPMNNGDEID  
 SLLNDROGTHMLDVMODHPSRASSIIBELPDREPTREPOPTHTYLPSPLRHRRPF  
 FPKPRIRASLMPSPREPLNHPNFOPLTEIHQAQMDIHFSBPAPQHPPTETRA  
 EBDDETYCRIRHNSSTGLRKQDCQDKRETLSDVCSSTNPSQAKLRRLDESLSVA  
 EELTRKYVELLSYVWKLNTSLLEQLNEQFNWVSLNLTQGBQVYLRATYTVASH  
 TSDSPVPSGVTEVVKLPDSDPIYTVFVPSVRKPKFMEYVABRALQYRKCHREB"

CDS

BASE COUNT 423 a 486 c 439 g 310 t  
 ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1658;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 CAGCAGCAGAGTCTTCATCAT 21  
 69 CAGCAGCAGAGTCTTCATCAT 49

Search completed: November 8, 2003, 01:49:34  
 Job time : 1412 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

1 nucleic - nucleic search, using sw model

on on: November 8, 2003, 02:40:54 ; Search time 1968 Seconds  
(without alignments)  
259.347 Million cell updates/sec

file: US-09-944-326-4

reference score: 21

oring table: 1 cagcagcagcagcctcatcat 21

arched: 22781392 seags, 12152238056 residues

tal number of hits satisfying chosen parameters: 124404

ntum DB seq length: 0

ximum DB seq length: 50

et-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

tabase :

EST.\*  
1: em\_estda.\*  
2: em\_esthum.\*  
3: em\_estlin.\*  
4: em\_estm.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gse\_hum.\*  
18: em\_gse\_hiv.\*  
19: em\_gse\_pln.\*  
20: em\_gse\_vrt.\*  
21: em\_gse\_fun.\*  
22: em\_gse\_mam.\*  
23: em\_gse\_mus.\*  
24: em\_gse\_pro.\*  
25: em\_gse\_rtd.\*  
26: em\_gse\_phg.\*  
27: em\_gse\_vr1.\*  
28: gb\_gse1.\*  
29: gb\_gse2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

ult No.	Score	Query Match	Length	ID	Description
1	14.8	70.5	46	9	AA916352 ch80e11.8
2	14.6	69.5	44	14	W25663 W25663
3	14	66.7	50	28	BH861678 BH861678
4	13	61.9	21	28	AZ802584 AZ802584

5	13	61.9	41	28	BH908888
6	13	61.9	43	9	AA973632
7	13	61.9	48	29	AL948370
8	12.8	61.0	46	9	AL649065
9	12.8	61.0	50	9	AU107924
10	12.8	61.0	50	9	AU107925
11	12.8	61.0	50	9	AU107928
12	12.8	61.0	50	9	AU107929
13	12.6	60.0	39	29	AL760945
14	12.6	60.0	43	9	AL766391
15	12.6	60.0	46	9	AA561123
16	12.6	60.0	46	14	CB213634
17	12.6	60.0	50	9	AU105963
18	12.6	60.0	50	9	AU105967
19	12.6	60.0	50	9	AU105968
20	12.6	60.0	50	9	AU105972
21	12.6	60.0	50	9	AA566984
22	12.4	59.0	37	28	AZ797149
23	12.2	58.1	35	28	AZ332831
24	12.2	58.1	43	28	AZ610505
25	12.2	58.1	46	9	AA109083
26	12.2	58.1	49	9	AA052336
27	12.2	58.1	49	9	AA864073
28	12.2	58.1	50	9	AU104442
29	12.2	57.1	33	28	AZ305164
30	12.2	57.1	33	28	AZ318599
31	12.2	57.1	34	9	AA116347
32	12.2	57.1	34	12	BI246596
33	12.2	57.1	35	29	BX285461
34	12.2	57.1	40	28	BH910804
35	12.2	57.1	41	29	BZ586362
36	12.2	57.1	46	14	H92446
37	12.2	57.1	46	14	T74174
38	12.2	57.1	47	28	AZ772648
39	12.2	57.1	49	9	AI197165
40	12.2	57.1	49	28	AQ025388
41	12.2	57.1	49	29	BZ582345
42	12.2	57.1	49	29	DME545293
43	12.2	57.1	50	9	AU103332
44	12.2	57.1	50	9	AU103352
45	12.2	57.1	50	9	AU107277

## ALIGNMENTS

RESULT 1  
AA916352  
LOCUS  
DEFINITION  
ch80e11.81 NCI CGAP C08 Homo sapiens CDNA clone IMAGE:147356 3'  
similar to TR:Q15347 Q15347 RAGA. [1] ; mRNA sequence.  
AA916352  
ACCESSION  
AA916352  
VERSION  
AA916352.1 GI:3055744  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM

REFERENCE  
AUTHORS  
TITLES  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Christopher Moskajuk, M.D., Ph.D., Michael R.  
Brunner-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Greg Lennon, Ph.D.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished

found through the I.M.A.G.E. Consortium/BLM at:  
www-bio.livl.gov/bbtp/image/image.html

Trace considered overall poor quality  
Seq primer: -40m13 fwd. Et from AmerSham  
High quality sequence stop: 1.  
Location/Qualifiers

TUES  
source

1. 46  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="IMAGE:1473356"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH108"  
/clone\_id="NCI\_CGAP\_Co8"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

B COUNT 11 a 12 c 8 g 15 t  
GIN

Query Match 70.5%; Score 14.8; DB 9; Length 46;  
Best Local Similarity 88.9%; Pred. No. 1e+04; 2; Indels 0; Gaps 0;  
atches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCAT 18  
|||||  
20 CAGCAGCTTACCTTCAT 37  
|||||

W25663 44 bp mRNA linear EST 25-NOV-1996  
z66608.k1 Soares fetal heart NBH19W Homo sapiens cDNA clone  
IMAGE:327110.5 similar to gb:U15183\_cdel HEAT SHOCK PROTEIN HSP  
90-ALPHA (HUMAN); mRNA sequence.  
W25663  
W25663.1 GI:1303517  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 44)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rittin, L., Rohlfing, T., Soares, M., Tan, P., Trevaaskis, E., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.  
The WashU-Merck EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
This clone is available royalty-free through LML; contact the IMGB Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Insert Length: 596 Std Error: 0.00  
Seq primer: mob.REGA+ET  
High quality sequence stop: 1.  
Location/Qualifiers

TUES  
source

1. 44  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:327110"  
/sex="unknown"

/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_id="Soares fetal heart NBH19W"  
/note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTACCAATCTGAGTGGAGCGCGCATCTTTTCTTTTCTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBH19W."

BASR COUNT 12 a 8 c 11 g 12 t 1 others  
ORIGIN

Query Match 69.5%; Score 14.6; DB 14; Length 44;  
Best Local Similarity 81.0%; Pred. No. 1.2e+04;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCAT 21  
|||||  
26 CAGCAGTGGCTTCAT 6  
|||||

RESULT 3  
BH861678/c  
LOCUS  
DEFINITION  
SALK\_087727 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK\_087727, genomic survey sequence.  
BH861678  
BH861678.1 GI:22097004  
GSS.  
Arabidopsis thaliana (chale crese)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; rosids  
euroids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 50)  
Alonso, J.M., Leteise, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrihab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shim, P., Zimmerman, J. and Ecker, J.R.  
A sequence-indexed library of Insertion Mutations in the Arabidopsis Genome  
Unpublished  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: eckers@salik.edu  
This is single pass sequence recovered from the left border of TDNA.  
Class: TDNA tagged.  
Location/Qualifiers

FEATURES  
source

1. 50  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone\_id="SALK\_087727"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"  
BASE COUNT 10 a 14 c 15 g 11 t

Query Match 66.7%; Score 14; DB 28; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+04;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 3 CCAGCAGAGCTCTTC 16  
 |||||  
 41 CCAGCAGAGCTCTTC 28

RESULT 4  
 A2802584 21 bp DNA linear GSS 16-FEB-2001  
 2M0061105R Mouse 10kb plasmid UGCM library Mus musculus genomic  
 clone UGCG2M0061105 R, genomic survey sequence.  
 A2802584  
 A2802584.1 GI:12954907  
 GSS.  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 21)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.  
 and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0061 row: 1 column: 05  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 21.  
 Location/Qualifiers  
 1..21  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCG2M0061105"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCM library"  
 /note="Vector: PWD2nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptor complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

RE COUNT

8 a 3 g 3 t

ORIGIN  
 Query Match 61.9%; Score 13; DB 28; Length 21;  
 Best Local Similarity 76.2%; Pred. No. 4.1e+04;  
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 1 CAGCAGCAGAGCTCTTCATCAT 21  
 |||||  
 1 CAGCAGCAGCATACATCATCAT 21

RESULT 5  
 BH908888 41 bp DNA linear GSS 04-SEP-2002  
 BH908888  
 LOCUS  
 DEFINITION  
 SALK\_051042.25.80.x Arabidopsis thaliana TDNA insertion lines  
 Arabidopsis thaliana genomic clone SALK\_051042.25.80.x, genomic  
 survey sequence.  
 BH908888  
 BH908888.1 GI:22721821  
 GSS.  
 Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
 1 (bases 1 to 41)  
 Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadgil,  
 C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,  
 Zimmerman, J., and Ecker, J.R.  
 A Sequence-indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 Unpublished  
 Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single-pass sequence recovered from the left border of  
 TDNA. This sequence lies within an annotated exon of At5g58140.  
 Class: TDNA tagged.  
 Location/Qualifiers  
 1..41  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_051042.25.80.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at http://signal.salk.edu/tdna\_protocols.html"

FEATURES  
 source  
 1..41  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_051042.25.80.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at http://signal.salk.edu/tdna\_protocols.html"

BASE COUNT  
 ORIGIN  
 Query Match 61.9%; Score 13; DB 28; Length 41;  
 Best Local Similarity 76.2%; Pred. No. 5.9e+04;  
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 1 CAGCAGCAGAGCTCTTCATCAT 21  
 |||||  
 19 CAGCAGGAGGATTTCTTACCAT 39

RESULT 6  
 AA973632 43 bp mRNA linear EST 17-JUN-1998  
 DEFINITION  
 AA973632  
 similar to SW:XPB\_CERRA P33194 POSSIBLE DNA-REPAIR PROTEIN XP-E ;

RNA sequence.  
 AA973632.1 GI:3148812  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 43)  
 NC1-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index.  
 Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NC1-CCAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
 Insert Length: 703 Std Error: 0.00  
 Seq Primer: -40m3 fwd. Et from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..43  
 /organism="Homo sapiens"  
 /mol\_type="RNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1569391"  
 /tissue\_type="carcinoid"  
 /lab\_host="DH10B"  
 /clone\_1lb="NC1-CCAP Luf"  
 /note="Organ: lung; Vector: pTT3D-Pac (pharmacia) with a  
 modified polylinker; 1st strand cDNA was prepared from  
 neuroendocrine lung carcinoid, and was then primed with a  
 Not I - oligo(dT) primer. Double-stranded cDNA was ligated  
 to Eco RI adaptor (pharmacia). digested with Not I and  
 cloned into the Not I and Eco RI sites of the modified  
 pTT3 vector. Library is normalized. Library was  
 constructed by Bento Soares and M. Patricia Bonaldi."

B COUNT 15 a 13 c 6 g 9 t  
 GIN

Query Match 61.9%; Score 13; DB 9; Length 43;  
 est Local Similarity 76.2%; Pred. No. 6.1e+04;  
 atches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 1 CAGCAGCAGAGCTTCATCAT 21  
 1 CACCATAGAGCTTCACCAT 21

UTR 7 48 bp DNA linear GSS 24-OCT-2002  
 US 48370/c  
 INITIATION Arabidopsis thaliana T-DNA flanking sequence GK-11H09-015792,  
 ESSION genomic survey sequence.  
 STION AL948370.1 GI:24404992  
 WORDS GSS.  
 RANISM Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1  
 Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.  
 and Weisshaar,B.

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 FEATURES  
 source  
 1..48  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone\_1lb="GK-11H09-015792"  
 /note="PCR was performed on DNA from Arabidopsis thaliana  
 plants (T1) which were transformed with the T-DNA from  
 vector PAC61. The lines contain one or more T-DNA  
 insertions. The DNA fragment(s) resulting from the PCR  
 were directly sequenced to determine the genomic sequence  
 flanking the insertion. Sequences displaying significant  
 similarity to the A. thaliana nuclear genome sequence were  
 processed for submission. T-DNA derived sequences were  
 removed"

BASE COUNT 14 a 7 c 14 g 13 t  
 ORIGIN

Query Match 61.9%; Score 13; DB 29; Length 48;  
 Best Local Similarity 76.2%; Pred. No. 6.5e+04;  
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 1 CAGCAGCAGAGCTTCATCAT 21  
 37 CAGCAGCAGAGCTTCATCAT 17

cy  
 Db

RESULT 8  
 AL649065  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Siliwana tropicalis (western clawed frog)  
 Siliwana tropicalis  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 Xenopodinae; Siliwana.  
 1 (bases 1 to 46)  
 Sanger Xenopus tropicalis EST project 2001 (10\_2001)  
 Unpublished  
 Contact: Huckle B  
 Sanger Centre  
 Hinxton, Cambridgeshire, CB10 1SA, UK  
 Email: [tropesanger.ac.uk](mailto:tropesanger.ac.uk)  
 Sanger Xenopus tropicalis EST project 2001  
 TROPICALIS\_SEQUENCE\_ID: Tsa034101.sp6

Sequencing primer: SP6

This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.

Location/Qualifiers

1..46

/organism="Silurana tropicalis"

/mol\_type="mRNA"

/db\_xref="taxon:8364"

/clone="TGA8034101"

/dev\_stages="gastrula (stages 10.5-13 mixed)"

/lab\_host="XGC-gastrula"

/clone\_lib="XGC-gastrula"

/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dT primed from Sug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."

ASB COUNT 10 a 14 c 11 g 11 t

ORIGIN

Query Match 61.0%; Score 12.8; DB 9; Length 46;

Best Local Similarity 87.5%; Pred. No. 7.7e+04; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 6 GCAGAGCTTCATCAT 21  
b 21 GCCGCGCTTCATCAT 36

ESUT 9  
U107924  
OCUS  
EXPUNTION  
AUI07924 50 bp mRNA linear EST 30-AUG-2001  
HRC02185, mRNA sequence.

CCBSSION  
AUI07924  
ERSON  
AUI07924.1 GI:13557446

EST.  
Homo sapiens (human)

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
1 (bases 1 to 50)  
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata  
, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki  
, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

EMBL  
21270072

11375929  
Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano  
, S. Construction and characterization of a full length-enriched and  
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

Location/Qualifiers  
1..50

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="HRC02185"  
/clone\_lib="Sugano Homo sapiens cDNA library"

ASB COUNT 10 a 15 c 21 g 4 t

ORIGIN

Query Match 61.0%; Score 12.8; DB 9; Length 50;  
Best Local Similarity 87.5%; Pred. No. 8.1e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
2 AGCAGCAGAGCTTCATCA 17

Db 27 AGCAGCAGAGCTTCATCA 42

RESULT 10  
AUI07925 50 bp mRNA linear EST 30-AUG-2001  
AUI07925 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
HRC02185, mRNA sequence.

DEFINITION  
AUI07925  
AUI07925  
AUI07925.1 GI:13557447

EST.  
Homo sapiens (human)

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
1 (bases 1 to 50)  
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata  
, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki  
, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

EMBL  
21270072

11375929  
Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano  
, S. Construction and characterization of a full length-enriched and  
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

Location/Qualifiers  
1..50

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="HS106916"  
/clone\_lib="Sugano Homo sapiens cDNA library"

ASB COUNT 10 a 15 c 19 g 6 t

ORIGIN

Query Match 61.0%; Score 12.8; DB 9; Length 50;  
Best Local Similarity 87.5%; Pred. No. 8.1e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 2 AGCAGCAGAGCTTCATCA 17  
b 27 AGCAGCAGAGCTTCATCA 42

ESUT 11  
U107928 50 bp mRNA linear EST 30-AUG-2001  
AUI07928 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
HRC02185, mRNA sequence.

DEFINITION  
AUI07928  
AUI07928  
AUI07928.1 GI:13557450

EST.  
Homo sapiens (human)

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
1 (bases 1 to 50)  
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata  
, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki  
, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

EMBL  
21270072

11375929

NAME: Yuraka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yuraka@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
 Location/Qualifiers  
 1. 50  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="ZRV62348"  
 /clone\_id="Sugano Homo sapiens cDNA library"

SB COUNT 10 a 15 c 20 g 5 c  
 IGIN

Query Match 61.0%; Score 12.8; DB 9; Length 50;  
 Best Local Similarity 87.5%; Pred. No. 8.1e+04;  
 Matches 1; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 AGCAGCAGAGCTCTCA 17  
 |||||  
 27 AGCAGCAGAGCTCCCA 42

SULT 12 50 bp mRNA linear EST 30-AUG-2001  
 CUS 107929  
 PINITION AU107929 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 ZRV62402, mRNA sequence.  
 CESSION AU107929  
 RSION AU107929.1 GI:13557451  
 YWORDS EST.  
 ORGANISM Homo sapiens (human)

PERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 50)  
 Suzuki, Y., Taira, H., Tanoda, T., Mizushima-Sugano, J., Sese, J., Hata  
 'H., Ota, T., Isegaki, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki  
 'Y., Nakamura, Y., Suyama, A. and Sugano, S.  
 Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites  
 EMBO Rep. 2 (5), 388-393 (2001)  
 21270072  
 11375929

TITLE Contact: Yuraka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yuraka@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
 Location/Qualifiers  
 1. 50  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="ZRV62402"  
 /clone\_id="Sugano Homo sapiens cDNA library"

SE COUNT 10 a 17 c 18 g 5 c  
 IGIN

Query Match 61.0%; Score 12.8; DB 9; Length 50;  
 Best Local Similarity 87.5%; Pred. No. 8.1e+04;  
 Matches 1; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 AGCAGCAGAGCTCTCA 17  
 |||||  
 29 AGCAGCAGAGTCCCA 44

RESULT 13 39 bp DNA linear GSS 18-JUN-2002  
 LOCUS AL760945/c  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-204B10-014508,  
 genomic survey sequence.  
 AL760945  
 AL760945.1 GI:21501350  
 GSS.  
 ORGANISM Arabidopsis thaliana (thale cress)

REFERENCE 1  
 Arabidopsis thaliana (thale cress)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.  
 1  
 Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., Saedler, H.  
 and Weishaar, B.  
 A pipeline for automated high-throughput generation of FSTs  
 (flanking sequence tags) from Arabidopsis thaliana T-DNA  
 transformed lines  
 Unpublished

REFERENCE 2  
 Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weishaar, B.  
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
 for flanking sequence tag based reverse genetics  
 Unpublished

REFERENCE 3 (bases 1 to 39)  
 Rosso, M., Li, Y., Strizhov, N. and Weishaar, B.  
 Direct Submision  
 Submitted (17-JUN-2002) Weishaar B., Max-Planck-Institut fuer  
 Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 This sequence is recovered from the left border of the T-DNA. It  
 indicates an insertion within the locus defined by clone t10j. The  
 sequences are generated at the MPI for Plant Breeding Research in  
 the context of the GABI-Kat project. GABI-Kat is part of the German  
 Plant Genomics program designated 'GABI'. Information on line  
 availability can be found at:  
 http://www.mpil-koeln.mpg.de/GABI-Kat/.

FEATURES  
 source  
 1. 39  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="GK-204B10-014508"  
 /clone\_id="Arabidopsis thaliana T-DNA insertion lines"  
 /note="PCR was performed on DNA from Arabidopsis thaliana  
 plants (T1) which were transformed with the T-DNA from  
 vector pAC161. The lines contain one or more T-DNA  
 insertions. The DNA fragment(s) resulting from the PCR  
 were directly sequenced to determine the genomic sequence  
 flanking the insertion. Sequences displaying significant  
 similarity to the A. thaliana nuclear genome sequence were  
 processed for submission. T-DNA derived sequences were  
 removed"

BASE COUNT 10 a 12 c 10 g 7 c  
 ORIGIN

Query Match 60.0%; Score 12.6; DB 29; Length 39;  
 Best Local Similarity 78.9%; Pred. No. 8.6e+04;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

2 AGCAGCAGAGCTCTCA 20  
 |||||  
 38 AGCAGCAGAGTCTCA 20

RESULT 14 43 bp mRNA linear EST 20-DEC-1999  
 LOCUS AT766391/c  
 DEFINITION wh6104.x1 NCI\_CGAP Kid11 Homo sapiens cDNA clone IMAGE:238523 3'  
 similar to SW-COX2\_HUMAN P00403 CYTOCHROME C OXIDASE POLYPEPTIDE II

;; mRNA sequence.  
 JSESSION A1766391  
 ERSION A1766391.1 GI:5232900  
 SYMORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 43)  
 NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapdb-remail.nih.gov](mailto:cgapdb-remail.nih.gov)  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Bamber-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
[www.bio.linn.gov/bdnp/image/image.html](http://www.bio.linn.gov/bdnp/image/image.html)  
 Trace considered overall poor quality  
 Insert Length: 641 Std Error: 0.00  
 Seq primer: -40UP from G1bco  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1. 43  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2385223"  
 /lab\_host="DH10B"  
 /clone\_1b="NCI CGAP\_Kid11"  
 /note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with  
 a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
 Plasmid DNA from the normalized library NCI\_CGAP\_Kid11 was  
 prepared, and 88 circles were made in vitro. Following HAP  
 purification, this DNA was used as tracer in a subtractive  
 hybridization reaction. The driver was PCR-amplified cDNAs  
 from a pool of 5,000 clones made from the same library  
 (cloneids 132376-132391). 1456007-145675, and  
 1500552-1502855). Subtraction by Bento Soares and M.  
 Fatima Bonaldo."  
 Feature Counts: 10 a 5 c 21 g 7 t  
 Query Match 60.0%; Score 12.6; DB 9; Length 43;  
 Best Local Similarity 78.9%; Pred. No. 9.1e+04;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 1. CAGCAGCAGGCTTCATC 19  
 |||||  
 32 CATCATCATGCTCTCATC 14  
 SUTR 15  
 561123/c  
 CUS AAS61123 46 bp mRNA linear EST 18-AUG-1997  
 PINITION V141C01.r1 Stragene mouse skin (#937313) Mus musculus cDNA clone  
 IMAGE:974784 5' similar to TR:G972037 G972037 SUCCINATE  
 DEHYDROGENASE ;, mRNA sequence.  
 CESSION AAS61123  
 RSION AAS61123.1 GI:2332588  
 YMORDS EST.  
 ORGANISM Mus musculus (house mouse)  
 URCE Mus musculus  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 46)  
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
 Schellenberg, K., Steproe, M., Tan, F., Underwood, K., Moore, B.,  
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
 Waterston, R.  
 The WashU-HMI Mouse EST Project  
 Unpublished  
 Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: [mouseest@wustl.edu](mailto:mouseest@wustl.edu)  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information.  
 MGI:555512  
 Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: -28ml3 rev1 RT from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1. 46  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:974784"  
 /sex="female"  
 /tissue\_type="whole skin"  
 /dev\_stage="11 weeks old"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /clone\_1b="Stragene mouse skin (#937313)"  
 /note="Organ: Skin; Vector: pBluescript SK-; Site 1: EcoRI  
 ; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo  
 dt. Whole skin from 11 week old C57BL/6 female mice.  
 Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'  
 adaptor sequence: 5' CTAATCGCAGCAG 3' -3' adaptor  
 sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."  
 Feature Counts: 11 a 11 c 15 g 9 t  
 Query Match 60.0%; Score 12.6; DB 9; Length 46;  
 Best Local Similarity 78.9%; Pred. No. 9.5e+04;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 1. CAGCAGCAGGCTTCATC 19  
 |||||  
 46 CAGCATCATGCTCTCATC 28  
 Db  
 Search completed: November 8, 2003, 03:50:17  
 Job time: 1973 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

1 nucleic - nucleic search, using sw model

on: November 8, 2003, 01:51:04 ; Search time 1422 Seconds

(without alignments)  
604.151 Million cell updates/sec

File: US-09-944-326-4

Sequence: 1 cagcagcagagctctcatcat 21

Indexing table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Marched: 2888711 seqs, 2045481386 residues

Cal number of hits satisfying chosen parameters: 1316618

Minimum DB seq length: 0

Minimum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: GenBank

- 1: gb\_ba:\*
- 2: gb\_hcg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_scs:\*
- 12: gb\_ey:\*
- 13: gb\_un:\*
- 14: gb\_vl:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_om:\*
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- 23: em\_pat:\*
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- 25: em\_pl:\*
- 26: em\_ro:\*
- 27: em\_scs:\*
- 28: em\_un:\*
- 29: em\_vl:\*
- 30: em\_hcg\_hum:\*
- 31: em\_hcg\_inv:\*
- 32: em\_hcg\_other:\*
- 33: em\_hcg\_mus:\*
- 34: em\_hcg\_pln:\*
- 35: em\_hcg\_rtd:\*
- 36: em\_hcg\_mam:\*
- 37: em\_hcg\_vrt:\*
- 38: em\_ey:\*
- 39: em\_hcg\_hum:\*
- 40: em\_hcg\_mus:\*
- 41: em\_hcg\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.2	77.1	32	6	AR274120
2	16.2	77.1	48	6	A76301
3	16.2	77.1	48	6	E01067
4	15.4	73.3	39	6	A08489
5	15.4	73.3	39	6	A12568
6	15.4	73.3	45	6	A05116
7	15.2	72.4	22	6	AX268965
8	14.8	70.5	27	6	AX118356
9	14.8	70.5	31	6	AR070079
10	14.8	70.5	31	6	AR258163
11	14.8	70.5	31	6	AK670795
12	14.6	69.5	48	6	A76303
13	14.4	68.6	39	6	A08490
14	14.4	68.6	39	6	A08491
15	14.4	68.6	39	6	A12569
16	14.4	68.6	39	6	A12570
17	14.2	67.6	20	6	AR085567
18	14.2	67.6	20	6	AR221110
19	14.2	67.6	22	6	AK697095
20	14.2	67.6	24	6	AR221229
21	14.2	67.6	26	6	AK697096
22	14.2	67.6	30	6	A70102
23	14.2	67.6	30	6	AR148235
24	14.2	67.6	30	6	AR204084
25	14.2	67.6	30	6	BD077090
26	14.2	67.6	47	6	AR291280
27	13.8	65.7	18	6	AR092800
28	13.8	65.7	37	6	A36373
29	13.8	65.7	37	6	AR070094
30	13.8	65.7	37	6	AR258178
31	13.8	65.7	37	6	AK670814
32	13.8	65.7	50	6	AX233374
33	13.6	64.8	20	6	AR230827
34	13.6	64.8	20	6	AR314013
35	13.6	64.8	20	6	BD064760
36	13.6	64.8	20	6	BD101829
37	13.6	64.8	23	6	AR234673
38	13.6	64.8	50	6	AR252583
39	13.6	64.8	50	6	AX080828
40	13.6	64.8	50	6	AX403425
41	13.4	63.8	20	6	AR221109
42	13.4	63.8	34	6	AR045234
43	13.4	63.8	34	6	I52286
44	13.2	62.9	18	6	AR085592
45	13.2	62.9	23	6	AX262444

ALIGNMENTS

RESULT 1	AR274120	32 bp	DNA	linear	PAT 10-APR-2003
LOCUS	AR274120				
DEFINITION	Sequence 6 from patent US 6504083.				
ACCESSION	AR274120				
VERSION	AR274120.1	GI:29706097			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 32)				
AUTHORS	Barbour,B., Meyer,T.B.C. and Saad,M.B.				
TITLE	Maize Gcs-2 promoters				
JOURNAL	Patent: US 6504083-A 6 07-JAN-2003;				
FEATURES	Location/Qualifiers				

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:GIN
Query Match     77.1%; Score 16.2; DB 6; Length 32;
Best Local Similarity 85.7%; Pred. No. 7.8e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21
  |||||
3 CAGCAGCAGAGTCTTCATCAT 23

:ULT 2
:301/c
:INITIATION     A76301      48 bp      DNA      linear      PAT 19-OCT-1999
:SSION          A76301
:SION           A76301.1 GI:6088388
:WORDS
:RCE            unidentified
:ORGANISM       unidentified
:REFERENCE      unclassified.
:AUTHORS        1 (bases 1 to 48)
:TITLE          Maegert,H.
:JOURNAL        DNA CODING FOR APHRODISIN
:               Patent: WO 9319173-A 7 30-SEP-1993;
:               FORSMANN WOLF GEORG (DE).
:FEATURES
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:   GIN
Query Match     77.1%; Score 16.2; DB 6; Length 48;
Best Local Similarity 85.7%; Pred. No. 7.6e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21
  |||||
21 CAGCAGCAGAGTCTTCATCAT 1

:ULT 3
:067/c
:INITIATION     E01067      48 bp      DNA      linear      PAT 29-SEP-1997
:SSION          E01067
:SION           E01067.1 GI:2169326
:WORDS          JP 1987000276-A/9
:RCE            Homo sapiens (human)
:ORGANISM       Homo sapiens
:               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
:               Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
:REFERENCE      Takiguchi,H., Furukawa,H. and Tanl,T.
:AUTHORS        PRODUCTION OF PANCREAS ELASTASE
:TITLE          Patent: JP 1987000276-A 9 06-JAN-1987;
:JOURNAL        SANKYO CO LTD NIPPON SODA CO LTD, NISSAN CHEM IND LTD, TOYO SODA
:               MFG CO LTD
:               OS homo sapiens (human)
:               PN JP 1987000276-A/9
:               PD 06-JAN-1987
:               PF 25-JUN-1985 JP 1985138494

```

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PI TAKIGUCHI HIROSHI, FURUKAWA HIDEHIKO, TANI TOKIO PC
C12N9/66,A61K35/74,A61K37/54,C12N15/00//C07H21/04,(C12N9/66, PC
C12R1.19)
PC (C12N15/00,C12R1.19);
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CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: tissue=pancreas;
FH Key Location/Qualifiers
FH sig_peptide 1.48
FT peptide'
FT /product='human pancreas elastase-2 signal' FT

FEATURES
source
location/Qualifiers
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7 a      13 c      14 g      14 t

BASE COUNT
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Query Match     77.1%; Score 16.2; DB 6; Length 48;
Best Local Similarity 85.7%; Pred. No. 7.6e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21
  |||||
21 CAGCAGCAGAGTCTTCATCAT 1

Db
RESULT 4
A08489
LOCUS          A08489      39 bp      DNA      linear      PAT 22-JUL-1993
DEFINITION    B.taurus gene for somatotropin, partial.
ACCESSION     A08489
VERSION       A08489.1 GI:410773
KEYWORDS      somatotropin.
SOURCE        Bos taurus (cow)
ORGANISM      Bos taurus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
               Bovidae; Bovinae; Bos.
REFERENCE     1 (bases 1 to 39)
AUTHORS       Harbour,G.C., Hoogerheide,J.G. and Garlick,R.L.
TITLE         Enhanced bioactivity of mammalian somatotropin through selective
               deamidation
JOURNAL       Patent: EP 0263206-A 5 13-APR-1988;
               THE UPJOHN COMPANY
FEATURES
source
location/Qualifiers
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BASE COUNT
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ORIGIN
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Best Local Similarity 94.1%; Pred. No. 1.9e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

4 CAGCAGAGTCTTCATCA 20
  |||||
12 CAGCAGAGTCTTCACCA 28

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UTL 5	2568	39 bp	DNA	linear	PAT 04-JAN-1994
UTS	A12568				
FINITION	Fragment of bovine somatotropin.				
SSION	A12568				
SSION	A12568.1	GI:488953			
WORDS					
ORGANISM	Bos taurus (cow)				
	Bos taurus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bos.				
	1 (bases 1 to 39)				
REFERENCE					
AUTHORS					
TITLE	ENHANCED BIOACTIVITY OF MAMMALIAN SOMATOTROPIN THROUGH SELECTIVE DEAMINATION				
JOURNAL	Patent: WO 8701708-A 5 26-MAR-1987;				
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atches	16;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;	
	4 CAGCAGAGCTTCATCA 20				
	12 CAGCAGAGCTTCACCA 28				
UTL 6					
116					
TS	A05116	45 bp	DNA	linear	PAT 04-MAY-1993
ITION	Oligonucleotide U7 for bovine growth hormone.				
SSION	A05116				
SION	A05116.1	GI:345003			
WORDS					
ORGANISM					
RCE					
ANCE	synthetic construct				
UTORS	synthetic construct				
ITL	artificial sequence.				
	1 (bases 1 to 45)				
	METHOD FOR THE PRODUCTION OF BOVINE GROWTH HORMONE USING A SYNTHETIC GENE				
CURNAL	Patent: WO 8805078-A 13 14-JUL-1988;				
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atches	16;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;	
	4 CAGCAGAGCTTCATCA 20				
	21 CAGCAGAGCTTCACCA 37				
UTL 7					
US	AX268965	22 bp	DNA	linear	PAT 29-OCT-2001
INATION	Sequence 46 from Patent WO0175165.				
SSIGN	AX268965				
ITION	AX268965.1	GI:16541984			
WORDS					

	SOURCE	synthetic construct	
	ORGANISM	synthetic construct	
	REFERENCE	artificial sequences.	
	AUTHORS	1 Mcconlogue,J.C., Games,K.D., Yednock,T.A., Hua,T., Messersmith,B. and Bard,P.	
	TITLE	Screening markers and methods for neurodegenerative disorders	
	JOURNAL	Patent: WO 0175165-A 46.11-OCT-2001;	
	FEATURES	Elan Pharmaceuticals, Inc. (US)	
	source	Location/Qualifiers	
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		/organism="synthetic construct"	
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Oy		1 CAGCAGCAGGCTTTCATCA 20	
	Db	2 CAGCAGCAGGCTTTCATCA 21	
	RESULT 8:		
	LOCUS	AX118356	27 bp DNA linear PAT 11-MAY-2001
	DEFINITION	Sequence 3479 from Patent W00129262.	
	ACCESSION	AX118356	
	VERSION	AX118356.1 GI:14035307	
	KEYWORDS		
	SOURCE		
	ORGANISM	synthetic construct	
		synthetic construct	
		artificial sequences.	
	REFERENCE	1	
	AUTHORS	Picoult-Newburg,L. and Pohl,M.	
	TITLE	Genotyping reagents, kits and methods of use thereof	
	JOURNAL	Patent: WO 0129262-A 3479 26-APR-2001;	
	FEATURES	Orchid Biosciences, Inc. (US)	
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	Matches	16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
Oy		2 AGCAGCAGAGCTTCATCA 20	
	Db	22 AGCAGCAGGTGTGCATCA 4	
	RESULT 9		
	LOCUS	AR070079	31 bp DNA linear PAT 18-FEB-2000
	DEFINITION	Sequence 35 from patent US 5691716.	
	ACCESSION	AR070079	
	VERSION	AR070079.1 GI:7220967	
	KEYWORDS		
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	ORGANISM	Unknown.	
	REFERENCE	Unclassified.	
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Best Local Similarity	93.8%;	Pred. No. 5.6e+04;		
Matches 15;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
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12 CAGCAGAGCTTCACC 27

SULT 14  
8491  
CUS A08491 39 bp DNA linear PAT 22-JUL-1993  
PINTION oligonucleotide 4.  
CESSION A08491  
RSION A08491.1 GI:413473  
WORDS  
URCE  
ORGANISM synthetic construct  
synthetic construct  
artificial sequences.  
PERENCE 1 (bases 1 to 39)  
AUTHORS Harbourn,G.C., Hoogerheide,J.G. and Garlick,R.L.  
TITLE Enhanced bioactivity of mammalian somatotropin through selective  
demethylation  
JOURNAL Patent: EP 0263206-A 7 13-APR-1988;  
THE UPJOHN COMPANY  
AUTHORS Location/Qualifiers  
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BE COUNT 8 a 11 c 10 g 10 t

Query Match 68.6%; Score 14.4; DB 6; Length 39;  
Best Local Similarity 93.8%; Pred. No. 5.6e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

4 CAGCAGAGCTTCATC 19  
|||||  
12 CAGCAGAGCTTCACC 27

ULT 15  
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1A12569 39 bp DNA linear PAT 04-JAN-1994  
INITIATION fragment of synthetic somatotropin.  
BSSION A12569  
SION A12569.1 GI:491409

WORDS  
RCE  
ORGANISM synthetic construct  
synthetic construct  
artificial sequences.  
ERENCE 1 (bases 1 to 39)

UTORS  
TITLE ENHANCED BIOACTIVITY OF MAMMALIAN SOMATOTROPIN THROUGH SELECTIVE  
DEAMINATION  
JOURNAL Patent: WO 8701708-A 6 26-MAR-1987;  
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BE COUNT 7 a 12 c 10 g 10 t

Query Match 68.6%; Score 14.4; DB 6; Length 39;  
Best Local Similarity 93.8%; Pred. No. 5.6e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Time: 1424 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compen Ltd.

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on on: November 8, 2003, 01:49:39 ; Search time 251 Seconds  
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file: US-09-944-326-4

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scoring table: IDENTITY NUC  
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searched: 2552756 seqs, 1349719017 residues

total number of hits satisfying chosen parameters: 2467832

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Maximum DB seq length: 50

post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	21	AAA94226
2	17.8	84.8	50	20	AAK24790
3	16.2	77.1	32	21	AAA09140
4	16.2	77.1	50	21	AAA11024
5	15.2	72.4	22	22	AA515291
6	15.2	72.4	40	21	AA236146
7	15	71.4	33	24	ABQ80863
8	14.8	70.5	21	21	AAA94223

9	14.8	70.5	21	21	AAA94224	Murine testosterone
10	14.8	70.5	27	22	AAH40683	SNP specific SNPE
11	14.8	70.5	30	20	AAZ12445	PCR primer used to
12	14.8	70.5	31	15	AAQ69972	5' sense leader ex
13	14.6	69.5	24	24	ABL61345	Naja naja atra sho
14	14.6	69.5	33	24	ABK49118	Human transcriptio
15	14.6	69.5	34	22	AAH79384	Plasmalemma regula
16	14.6	69.5	44	20	AAK05964	Bacillus licheniflo
17	14.4	68.6	30	25	ABZ77331	Nucleotide sequenc
18	14.2	67.6	20	24	AAZ31857	PCR primer for hum
19	14.2	67.6	20	24	ABK69555	Rat phosphorlyase
20	14.2	67.6	22	21	AAK58494	Human PRO1283 (UNO
21	14.2	67.6	22	21	AAA37208	Human PRO1283 forw
22	14.2	67.6	22	22	AAK54314	Human PRO1283 forw
23	14.2	67.6	24	20	AAK08676	Primer #40 used in
24	14.2	67.6	24	22	AAK73404	Oligonucleotide de
25	14.2	67.6	26	21	AAK58495	Grand fir monoterp
26	14.2	67.6	26	21	AAA37209	Human PRO1283 (UNO
27	14.2	67.6	26	22	AAK54315	Human PRO1283 forw
28	14.2	67.6	30	20	AAK19511	Primer #41 used in
29	14.2	67.6	34	18	AAK6354	Human lipocalin ho
30	13.8	65.7	18	21	AAZ57675	Lambda primer 3.
31	13.8	65.7	28	24	ABK14351	Human G-alpha-12 a
32	13.8	65.7	30	22	AAK28287	Oligonucleotide 5'
33	13.8	65.7	31	14	AAK47780	PCR primer Lam B8
34	13.8	65.7	36	22	AAK56649	Human interleukin-
35	13.8	65.7	36	22	AAK56654	Human interleukin-
36	13.8	65.7	36	22	AAK56656	Human interleukin-
37	13.8	65.7	36	22	AAK56658	IL-11-IgG1-PC dire
38	13.8	65.7	41	22	AAK28289	Modified Gcc donor
39	13.8	65.7	50	22	AAK43508	Cornodesmosin sin
40	13.6	64.8	20	20	AAK55224	PCR primer used to
41	13.6	64.8	20	22	AAK54566	Human PAMP-1 anti
42	13.6	64.8	23	21	AAK69796	3' RT-PCR primer u
43	13.6	64.8	24	24	ABK10729	SV40 RT-PCR primer
44	13.6	64.8	27	14	AAK40995	Annealing oligonuc
45	13.6	64.8	32	20	AAK25040	Cyclin-dependent K

## ALIGNMENTS

RESULT 1	AAA94226	standard; DNA; 21 BP.
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AC	AAA94226;	
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DT	12-JAN-2001	(first entry)
XX		
DB	Human testosterone-repressed prostate message-2	antisease oligo #2.
XX		
KW	Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;	
KW	sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.	
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OS	Homo sapiens.	
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PN	WO200049937-A2.	
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PD	31-AUG-2000.	
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PF	25-FEB-2000; 2000WO-US04875.	
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PR	26-FEB-1999; 99US-0121726.	
XX		
PA	(UTBR-) UNIV BRITISH COLUMBIA.	
XX		
FI	Gleaves M, Rennie PS, Miyake H, Nelson C,	
XX		
DR	WPI; 2000-533132/48.	
XX		
PT	Treating prostatic tumors and renal cancers by antisense inhibition of	
PT	the testosterone-repressed prostate messenger-2 gene.	

Claim 3; Page 36; 38pp; English.

The present sequence is an antisense oligonucleotide directed at the human testosterone-repressed prostate message-2 (TRPM-2), also known as clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to promote the regression of tumours, and oligonucleotides directed at human TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2 gene. These include prostate cancer, renal cell cancer and some breast cancer cells. In addition to this, they also increase the chemosensitivity of the cells, meaning that conventional chemotherapy is more effective.

Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

1 CAGCAGCAGAGCTTCATCAT 21
|||||
1 CAGCAGCAGAGCTTCATCAT 21

```

ULT 2  
(24790/c  
AAx24790 standard; DNA; 50 BP.

AAx24790;

21-JUN-1999 (first entry)

Interleukin-18 binding protein splice variant IL-18BPA PCR primer.

Interleukin-18 binding protein; IL-18BP; IL-18BPA; splice variant; human; autoimmune disease; inflammation; diabetes; pancreatitis; rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis; psoriasis; inflammatory bowel disease; multiple sclerosis; ischemic heart disease; ischemic brain injury; gene therapy; PCR; primer; ss.

Synthetic.  
Homo sapiens.

WO9909063-A1.

25-FEB-1999.

13-AUG-1998; 98MO-1100379.

22-JUL-1998; 98IL-0125463.

14-AUG-1997; 97IL-0121554.

27-AUG-1997; 97IL-0121639.

29-SEP-1997; 97IL-0121860.

06-NOV-1997; 97IL-0122134.

(YEDA ) YEDA RES & DEV CO LTD.

Dinarello C, Kim SH, Novick D, Rubinstein M;

WPI; 1999-180975/15.

New interleukin-18 binding protein - useful for treating human diseases, including autoimmune disease and inflammation

Example 7; Page 39; 100pp; English.

The present sequence is a reverse primer that was used with a forward primer (see AAx24754) in the PCR amplification of the coding region of a cDNA clone (see AAx24749) coding for human interleukin-18 binding protein splice variant IL-18BPA (see AA98004). The PCR products were cut with XbaI and cloned into the XbaI site of the pEF-BOS expression vector. IL-BP18a was expressed in transfected

CC COS7 cells. The invention provides IL-18BP polypeptides capable of  
CC binding IL-18 and/or modulating and/or blocking IL-18 activity.  
CC These can be used to treat conditions requiring the protein  
CC (claimed), such as autoimmune diseases, type I diabetes, rheumatoid  
CC arthritis, graft rejections, inflammatory bowel disease, sepsis,  
CC multiple sclerosis, ischemic heart diseases, ischemic brain injury,  
CC chronic hepatitis, psoriasis, and chronic/acute pancreatitis.  
XX

SO Sequence 50 BP; 13 A; 8 C; 13 G; 16 T; 0 other;

Query Match 84.8%; Score 17.8; DB 20; Length 50;  
Best Local Similarity 90.5%; Pred. No. 1.2e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

OY 1 CAGCAGCAGAGCTTCATCAT 21
|||||
DB 42 CAGCAGCAGAGCTTCATCAT 22

```

RESULT 3  
AAA09140  
ID AAA09140 standard; DNA; 32 BP.

AC AAA09140;

DT 10-AUG-2000 (first entry)

DE Gos-2 promoter gene-specific primer 1.

KW maize; promoter; actin-2; enolase; Gos-2; L41; gene expression;  
KW regulation; plant transformation; primer; ss.

OS Zea mays.

PN WO200020571-A2.

PD 13-APR-2000.

PF 05-OCT-1999; 99MO-US23081.

PR 06-OCT-1998; 98US-0103294.

PR 05-NOV-1998; 98US-0107201.

PA (PION-) PIONEER HI-BRED INT INC.  
PA (AGER-) AGERI AGRIC GENETIC ENG RES INST.

PI Barbour E, Meyer TE, Saad ME;

DR WPI; 2000-303763/26.

Novel maize promoters used for producing transgenic plants with  
regulated expression of heterologous nucleotide sequences

Example 1; Page 26; 48pp; English.

CC Novel maize promoters (AAA09134-37) that drive expression of actin-2,  
CC enolase, Gos-2 or L41, respectively, were isolated from genomic DNA  
CC using PCR. The first round of PCR was performed on each DNA sample  
CC using PCR. The first round of PCR was performed on each DNA sample  
CC Clontech primer API (AAA09138) and a gene-specific primer 1  
CC (AAA09143) and a second round of PCR using Clontech primer API  
CC sequenced for verification and then amplified with Clontech primer AP3  
CC (AAA09148) and a gene-specific primer (AAA09149-52). The promoters are  
CC used for regulating the expression of heterologous nucleotide sequences  
CC to vary the phenotype of a plant, e.g. modifying fatty acid composition,  
CC altering amino acid content and altering the pathogen defense system of  
CC the plant. Plants comprising important commercial traits can be  
CC generated.

SO Sequence 32 BP; 8 A; 12 C; 6 G; 6 T; 0 other;

Query Match 77.1%; Score 16.2; DB 21; Length 32;

Best Local Similarity 85.7%; Pred. No. 5.3e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTTCATCAT 21  
|||||  
3 CAGCAGCAGAGCTTTCATCAT 23

SULT 4  
A11024/c  
AAA11024 standard; DNA; 50 BP.

AAA11024;

28-UTL-2000 (first entry)

Human mature Interleukin 18 binding protein coding sequence primer #2.

Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;  
regulator; drug; sensitivity disease; organ rejection; organ transplant;  
autoimmune disease; PCR primer; ss.

Homo sapiens.

MO200012555-A1.

09-MAR-2000.

18-NOV-1998; 98WC-JP05186.

01-SEP-1998; 98JP-0247588.

18-NOV-1998; 98JP-0327914.

(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

Torigoe K, Tanai M, Kurimoto M;

WPI 2000-237850/20.

Interleukin 18-binding protein with activity of regulating  
physiological actions of interleukin 18, useful as regulator and drug  
for sensitivity disease and organ rejection and in treating diseases  
due to excess immune reaction

Example 2; Page 22; 71pp; Japanese.

The invention relates to novel interleukin 18 (IL-18)-binding proteins  
from humans or mice which act as regulators and drugs for sensitivity  
diseases and organ rejection and in treating diseases due to excess  
immune reaction, e.g. in slowing down rejection after organ transplant,  
and in treating autoimmune diseases. This sequence represents a PCR  
primer used to isolate the coding sequence for the human mature  
interleukin 12 binding protein (AAA11002).

Sequence 50 BP; 7 A; 11 C; 18 G; 14 T; 0 other;

Query Match 77.1%; Score 16.2; DB 21; Length 50;  
Best Local Similarity 85.7%; Pred. No. 6.3e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTTCATCAT 21  
|||||  
44 CAGCAGCAGAGCTTTCATCAT 24

UTL 5

15291

AA15291 standard; DNA; 22 BP.

AA15291;

16-JAN-2002 (first entry)

DB Mouse IL-12 p40 #1 PCR primer 662F.

KW Mouse; ss; PCR primer; neurotrophic; neuroprotective; 662F;  
KW antiinflammatory; interleukin-1beta; IL-1b; tumour necrosis factoralpha;  
KW TNFalpha; macrophage inflammatory protein-1alpha; MIP-1alpha;  
KW fractalkine; glial fibrillar associated protein; GFAP; MHC; CX3CR1; CD86;  
KW major histocompatibility complex; Alzheimer's disease; cerebral ischaemia;  
KW neurodegenerative disease; VLDL-24OHase; MCP-1; IL-10; IL-12 p40;  
KW IFN-gamma; CD3 epsilon; CD4; IgG-1; Ig k; osteopontin.

Mus sp.

MO200175165-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US10247.

30-MAR-2000; 2000US-193847P.

(ELAN) ELAN PHARM INC.

McConlogue LC, Games KD, Yednock TA, Hua T, Messersmith E, Bard F;

WPI; 2001-639367/73.

Selecting compounds useful for treating or preventing Alzheimer's  
disease, from their ability to reduce levels of specific disease  
markers in animal models

Example 5; Page 23; 36pp; English.

The invention relates selecting compounds that reduce symptoms of  
Alzheimer's disease using a non-human mammal that has been subjected to  
cerebral ischaemia or lesion of a nerve so as to produce, in the  
affected region, increased levels of specific markers of Alzheimer's  
disease-associated inflammation. Test compounds are selected if they  
reduce levels of these markers significantly, in the affected region,  
relative to controls. The markers are interleukin-1beta (IL-1b), tumour  
necrosis factoralpha (TNFalpha), macrophage inflammatory protein-1alpha  
(MIP-1alpha), glial fibrillar associated protein (GFAP), MHC (major  
histocompatibility complex) Ialpha or II b, CD86, fractalkine or CX3CR1  
(a receptor for fractalkine). The method is used to identify compounds  
useful in treatment or prevention of Alzheimer's disease or other  
neurodegenerative diseases that have an inflammatory component. The  
method provides fast, accurate and quantitative drug screens. The  
present sequence is a PCR primer used to determine the level of  
a transcript for an efficacy marker in a transgenic mouse which  
overexpresses APP and displays Alzheimer's like neuropathy. The  
efficacy markers are VLDL-24OHase, MCP-1, IL-10, IL-12 p40, #1/#2,  
IFN-gamma #1/#2, CD3 epsilon, CD4 #1/#2, IgG-1, Ig k (light chain).

Sequence 22 BP; 6 A; 8 C; 3 G; 5 T; 0 other;

Query Match 72.4%; Score 15.2; DB 22; Length 22;  
Best Local Similarity 85.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

0Y 1 CAGCAGCAGAGCTTTCATCA 20  
|||||  
Db 2 CAGCAGCAGAGCTTTCATCA 21

RESULT 6

AA296146/c

ID AA296146 standard; DNA; 40 BP.

AA296146;

10-APR-2000 (first entry)

Polynucleotide sequence including binding site for BamHI.





The present sequence is an antisense oligonucleotide directed at the murine testosterone-repressed prostate message-2 (TRPM-2), also known as clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to promote the regression of tumours in mice, and oligonucleotides directed at human TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2 gene. These include prostate cancer, renal cell cancer and some breast cancer cells. In addition to this, they also increase the chemosensitivity of the cells, meaning that conventional chemotherapy is more effective.

Sequence 21 BP; 7 A; 5 C; 5 G; 4 T; 0 other;

Query Match 70.5%; Score 14.8; DB 21; Length 21;  
Best Local Similarity 88.9%; Pred. No. 2.4e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCAT 18  
|||||  
4 CAGCAGCAGAGCTTCAT 21

SULT 9  
AAA94224 standard; DNA; 21 BP.

AAA94224;

12-JAN-2001 (first entry)

Murine testosterone-repressed prostate message-2 antisense control.

Mouse; testosterone-repressed prostate message-2; TRPM-2; clusterin; sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.

Mus sp.

WO200049937-A2.

31-AUG-2000.

25-FEB-2000; 2000WO-US04875.

26-FEB-1999; 99US-0121726.

(UYBR-) UNIV BRITISH COLUMBIA.

Gleave M, Rennie PS, Miyake H, Nelson CJ;

WPI; 2000-533132/48.

Treating prostatic tumors and renal cancers by antisense inhibition of the testosterone-repressed prostate messenger-2 gene -

Example 1; Page 35; 38pp; English.

The present sequence is a mismatch control used with an antisense oligonucleotide directed at the murine testosterone-repressed prostate message-2 (TRPM-2, also known as clusterin, sulfated glycoprotein-2 or SGP-2). The antisense sequence was shown to promote the regression of tumours in mice, and similar oligonucleotides directed at human TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2 gene. These include prostate cancer, renal cell cancer and some breast cancer cells. In addition to this, they also increase the chemosensitivity of the cells, meaning that conventional chemotherapy is more effective.

Sequence 21 BP; 6 A; 6 C; 5 G; 4 T; 0 other;

Query Match 70.5%; Score 14.8; DB 21; Length 21;  
Best Local Similarity 88.9%; Pred. No. 2.4e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCAT 18

Db 4 CAGCAGCAGAGCTTCAT 21

RESULT 10  
AAH40683/c  
ID AAH40683 standard; DNA; 27 BP.  
XX  
AC AAH40683;

14-AUG-2001 (first entry)

SNP specific SNPB primer SEQ ID 3479.

Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPB; genotyping; agammaglobulinemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; primer; ss.

Homo sapiens.

WO200129262-A2.

26-APR-2001.

13-OCT-2000; 2000WO-US28436.

15-OCT-1999; 99US-0160096.

(ORCH-) ORCHID BIOSCIENCES INC.

Picoult-Newburg L, Pohl M;

WPI; 2001-290930/30.

New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polymorphic nucleotide polymorphism in a nucleic acid sample

Claim 1; Page 67; 83pp; English.

Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide primer extension (SNPB) primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a SNP flanking sequence, the SNPB primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolemia, polycystic kidney disease, osteogenesis imperfecta and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial disease of which a component is or may be genetic, such as autoimmune diseases, including, rheumatoid arthritis, multiple sclerosis, inflammation, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and paternity analysis. The present sequence represents a single nucleotide primer extension (SNPB) primer specific for a human SNP containing DNA sequence.

Sequence 27 BP; 5 A; 8 C; 4 G; 9 T; 1 other;

Query Match 70.5%; Score 14.8; DB 22; Length 27;  
Best Local Similarity 84.2%; Pred. No. 2.5e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

2 AGCAGCAGCTTCATCA 20  
|||||  
22 AGCAGCAGCTTCATCA 4

ULF 11  
12445/C  
AAZ12445 standard; DNA; 30 BP.

AAZ12445;

08-OCT-1999 (first entry)

PCR primer used to amplify ORF3 of *Neisseria* species.

*Neisseria meningitidis*; *Neisseria gonorrhoeae*; antigen; vaccine; treatment; *Neisseria* infection; meningitis; septicemia; gonorrhea; PCR primer; ss.

Synthetic.  
*Neisseria* sp.

MO9924578-A2.

20-MAY-1999.

09-OCT-1998; 98MO-IB01665.

01-SEP-1998; 98GB-0019016.  
06-NOV-1997; 97GB-0023516.  
14-NOV-1997; 97GB-0024190.  
18-NOV-1997; 97GB-0024386.  
27-NOV-1997; 97GB-0025158.  
10-DEC-1997; 97GB-0026147.  
14-JAN-1998; 98GB-0000759.

(CHIR-) CHIRON SPA.

Grandi G, Maignant V, Piazza M, Rappuoli R, Scarlato V;

WPI; 1999-327407/27.

Proteins from *Neisseria meningitidis* and *N. gonorrhoeae* useful for diagnosis, treatment and prevention of infection.

Disclosure; Page 489; 524p; English.

PCR primers AAZ12359-212531 were used to amplify various open reading frames (ORFs) of *Neisseria meningitidis* and *N. gonorrhoeae*. These ORFs (AAZ11972-212358) encode antigenic proteins (AAV38499-Y38944). The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of *Neisseria* infections, such as meningitis, septicemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.

Sequence 30 BP; 7 A; 10 C; 7 G; 6 T; 0 other;

Query Match 70.5%; Score 14.8; DB 20; Length 30;  
Best Local Similarity 88.9%; Pred. No. 2.5e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CAGCAGCAGCTTCAT 18  
|||||  
29 CAGCAGCAGCTTCAT 12

LT 12

:9972/C  
AA069972 standard; CDNA; 31 BP.

AA069972;

XX 25-MAR-2003 (updated)  
DT 13-MAR-1995 (first entry)  
XX

5'sense leader ex oligo primer to amplify 5' end Can fi cDNA.

XX Canis familiaris; protein allergen; dog dander; dog hair; allergy;  
KW T cell response; stimulation; diagnosis; sensitivity; therapeutic;  
KW agents; PCR; polymerase chain reaction; primer; amplification;  
KW probe; hybridisation; partial cDNA; degenerate; ss.

XX Synthetic.

XX MO9416068-A2.

XX 21-JUL-1994.

XX 30-DEC-1993; 93MO-US12468.

XX 31-DEC-1992; 92US-0999712.

XX 22-NOV-1993; 93US-0156549.

XX (IMMU-) IMMUNOLOGIC PHARM CORP.

XX Bizenkauskas CB, Brauer AM, Konieczny A, Morgenstern JP;

XX WPI; 1994-249215/30.

XX DNA encoding dog dander allergenic peptide(s) Can fi I and Can fi

XX IT - used in the diagnosis and treatment of sensitivity to dog

XX dander

XX Example 2; Page 59; 124p; English.

XX AA069972 is a 5' primer corresponding to residues -26 to -20 of Canfi  
(AAK5987). It is used with AA069973 to amplify and sequence the 5' end  
of the Can fi cDNA. Peptides of the invention have the ability to  
induce a T cell response, which may include T cell stimulation or  
T cell nonresponsiveness. Some have the ability to bind the dog  
dander specific IgE of dog dander allergic subjects. These peptides  
are useful in diagnosing sensitivity to dog dander. Other peptides  
significantly reduce the ability to bind dog dander allergic IgE and  
are thus useful as therapeutic agents. (See also AA069951-070006 and  
AAK5987-60018 - these include primers, and probes for isolation of  
cDNA coding Can fi and fiI allergens and peptides derived from the  
sequences.)  
XX (updated on 25-MAR-2003 to correct PN field.)

XX Sequence 31 BP; 7 A; 13 C; 5 G; 6 T; 0 other;

Query Match 70.5%; Score 14.8; DB 15; Length 31;  
Best Local Similarity 88.9%; Pred. No. 2.5e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 AGCAGCAGCTTCATC 19  
|||||  
Db 24 AGCAGCAGCTTCATC 7

RESULT 13  
ABL61345/C  
ID ABL61345 standard; DNA; 24 BP.

XX ABL61345;

XX 13-SEP-2002 (first entry)

XX Naja naja atra short chain neurotoxin-associated PCR primer #1.

XX Chinese cobra; neurotoxin; cancer; PCR; primer; ss.

XX Naja naja atra.

PN CN1337404-A.  
 PD 27-FEB-2002.  
 XX 03-AUG-2000; 2000CN-0119561.  
 PF 03-AUG-2000; 2000CN-0119561.  
 XX 03-AUG-2000; 2000CN-0119561.  
 PR (SHAN-) SHANGHAI BIOENGINEERING RES CENT CHINESE.  
 PA Cal Q, Yang S, Gong Y,  
 PI WPI; 2002-384228/42.  
 XX Short-chain nervous cobra toxin, its preparation and use -  
 XX Example 1; Page 11; 30pp; Chinese.  
 XX This invention describes a novel cobra short chain neurotoxin, the  
 XX polynucleotide encoding the polypeptide and the method for producing the  
 XX polypeptide by means of recombination technology. The invention also  
 XX discloses the method for curing several diseases, such as cancer, by  
 XX using the cobra short chain neurotoxin, and a medicine composite  
 XX containing the cobra short chain neurotoxin. This sequence represents a  
 XX PCR primer used in the amplification of the short chain neurotoxin  
 XX described in the method of the invention.  
 XX Sequence 24 BP; 7 A; 5 C; 6 G; 6 T; 0 other;  
 XX  
 XX Query Match 69.5%; Score 14.6; DB 24; Length 24;  
 XX Best Local Similarity 81.0%; Pred. No. 3e+03;  
 XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 XX  
 XX 1 CAGCAGCAGAGCTTTCATCAT 21  
 XX 21 CAGCAGCAGAGCTTTCATCTT 1  
 XX  
 XX RESULT 14  
 XX BK49118/c  
 XX D ABK49118 standard; DNA; 33 BP.  
 XX C ABK49118;  
 XX 02-JUL-2002 (first entry)  
 XX Human transcription factor LCR-F19.02 PCR primer #1.  
 XX Human; 88; transcription factor; LCR-F19.02; erythropathy; PCR; primer.  
 XX Homo sapiens.  
 XX MO200220583-A1.  
 XX 14-MAR-2002.  
 XX 25-JUN-2001; 2001MO-CN01053.  
 XX 28-JUN-2000; 2000CN-0116822.  
 XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
 XX Mao Y, Xie X;  
 XX WPI; 2002-351761/38.  
 XX Homo transcription factor F19.02 and encoding polynucleotide, used in  
 XX treatment of erythropathy -  
 XX Example 4; Page 18; 38pp; Chinese.  
 XX The invention relates to an isolated polypeptide of human (HOMO)  
 XX transcription factor LCR-F19.02 the cDNA encoding it, and its fragment,

CC analogue or derivative. Also included are vectors expressing the protein,  
 CC a host cell comprising the vector, the isolation of modulators of the  
 CC protein and an anti-transcription factor LCR-F19.02 antibody. The protein  
 CC and nucleic acid are used in diagnosis and treatment of erythropathy.  
 CC The present sequence is a PCR primer used to clone the cDNA encoding  
 CC transcription factor LCR-F19.02.  
 XX  
 XX Sequence 33 BP; 7 A; 9 C; 8 G; 9 T; 0 other;  
 XX  
 XX Query Match 69.5%; Score 14.6; DB 24; Length 33;  
 XX Best Local Similarity 81.0%; Pred. No. 3.1e+03;  
 XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 XX  
 XX 1 CAGCAGCAGAGCTTTCATCAT 21  
 XX 27 CAGCAGCAGAGCTTTCATCAT 7  
 XX  
 XX RESULT 15  
 XX AAH79384/c  
 XX ID AAH79384 standard; DNA; 34 BP.  
 XX AC AAH79384;  
 XX 04-DEC-2001 (first entry)  
 XX DE Plasmolemma regulation function-contained protein 70 cDNA PCR primer #3.  
 XX KM Plasmolemma regulation function-contained protein 70; cancer; HIV;  
 XX infection; gene therapy; human; PCR primer; 88.  
 XX OS Homo sapiens.  
 XX PN CN1302889-A.  
 XX PD 11-JUL-2001.  
 XX PF 29-OCT-1999; 99CN-0119927.  
 XX PR 29-OCT-1999; 99CN-0119927.  
 XX PA (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.  
 XX PI Mao Y, Xie Y;  
 XX WPI; 2001-566050/64.  
 XX PT Polypeptide-human protein 70 containing plasmolemma regulation function  
 XX and polynucleotide for coding it -  
 XX Example 5; Page 15(Disclosure); 27pp; Chinese.  
 XX CC The present invention provides the protein and coding sequences of human  
 XX CC plasmolemma regulation function-contained protein 70. The sequences can  
 XX CC be used in the treatment of cancer and HIV infection. The present  
 XX CC sequence is a PCR primer for the coding sequence of the invention.  
 XX Sequence 34 BP; 5 A; 9 C; 9 G; 11 T; 0 other;  
 XX  
 XX Query Match 69.5%; Score 14.6; DB 22; Length 34;  
 XX Best Local Similarity 81.0%; Pred. No. 3.1e+03;  
 XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 XX  
 XX 1 CAGCAGCAGAGCTTTCATCAT 21  
 XX 27 CAGCAGCAGAGCTTTCATCAT 7

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on: November 8, 2003, 02:44:45 ; Search time 69 Seconds  
(without alignments)

134.334 Million cell updates/sec

file: US-09-944-326-4

reference: 1 cagcagcagagctctcatcat 21

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imum DB seq length: 50

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Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/prodata/2/ina/5A\_COMB.seq:\*

4: /cgn2\_6/prodata/2/ina/5B\_COMB.seq:\*

5: /cgn2\_6/prodata/2/ina/5A\_COMB.seq:\*

6: /cgn2\_6/prodata/2/ina/5B\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

ult No.	Score	Query Match	Length	DB ID	Description
1	16.2	77.1	32	4	US-09-410-935B-6
2	15.4	73.3	45	1	US-07-885-689A-7
3	14.8	70.5	31	2	US-08-467-603-35
4	14.8	70.5	31	2	US-08-467-793-35
5	14.8	70.5	31	2	US-08-491-861A-35
6	14.8	70.5	31	4	US-09-374-671A-35
7	14.6	69.5	44	3	US-09-110-959A-11
8	14.2	67.6	20	4	US-09-205-860-3
9	14.2	67.6	20	4	US-09-657-452A-163
10	14.2	67.6	24	4	US-09-360-545-57
11	14.2	67.6	30	3	US-09-130-663-10
12	14.2	67.6	30	3	US-09-432-335-10
13	14.2	67.6	30	3	US-09-254-023B-20
14	14.2	67.6	30	3	US-09-614-022-10
15	14.2	67.6	47	4	US-09-422-978-3015
16	13.8	65.7	18	2	US-09-256-496-15
17	13.8	65.7	37	2	US-08-467-603-54
18	13.8	65.7	37	2	US-08-466-793-54
19	13.8	65.7	37	2	US-08-491-861A-54
20	13.8	65.7	37	4	US-09-374-671A-54
21	13.6	64.8	20	4	US-09-517-467B-87
22	13.6	64.8	20	4	US-09-198-452A-4550
23	13.6	64.8	23	4	US-09-489-085A-6
24	13.6	64.8	27	6	5463174-1
25	13.6	64.8	50	4	US-09-996-243-312
26	13.4	63.8	20	4	US-09-657-452A-162
27	13.4	63.8	34	1	US-08-373-124A-27

C	28	13.4	63.8	34	1	US-08-435-628-27	Sequence 27, Appl
C	29	13.2	62.9	18	2	US-09-205-860-28	Sequence 28, Appl
C	30	13.2	62.9	24	4	US-09-442-099A-9	Sequence 9, Appl
C	31	13.2	62.9	24	4	US-09-612-342-9	Sequence 9, Appl
C	32	13.2	62.9	24	4	US-08-343-443B-100	Sequence 100, Appl
C	33	13.2	62.9	38	3	US-09-130-663-26	Sequence 26, Appl
C	34	13.2	62.9	38	3	US-09-432-335-26	Sequence 26, Appl
C	35	13.2	62.9	38	4	US-09-614-022-26	Sequence 26, Appl
C	36	13.2	62.9	47	4	US-09-422-978-626	Sequence 26, Appl
C	37	13.2	61.9	19	4	US-08-422-978-7130	Sequence 26, Appl
C	38	13.2	61.9	23	1	US-08-390-850-363	Sequence 363, Appl
C	39	13.2	61.9	23	1	US-08-435-634-93	Sequence 93, Appl
C	40	13.2	61.9	31	1	US-08-390-850-94	Sequence 94, Appl
C	41	13.2	61.9	31	1	US-08-390-850-95	Sequence 95, Appl
C	42	13.2	61.9	31	1	US-08-435-634-93	Sequence 93, Appl
C	43	13.2	61.9	31	1	US-08-435-634-94	Sequence 94, Appl
C	44	13.2	61.9	31	1	US-08-435-634-94	Sequence 94, Appl
C	45	13.2	61.9	31	1	US-08-435-634-95	Sequence 95, Appl

## ALIGNMENTS

```

RESULT 1
US-09-410-935B-6
; Sequence 6, Application US/09410935B
; Patent No. 6504083
; GENERAL INFORMATION:
; APPLICANT: Barbour, Eric
; APPLICANT: Enclaire Meyer, Terry
; APPLICANT: Ridd, Saad, Mohammed
; TITLE OR INVENTION: No. 6504083el Maize Promoters
; FILE REFERENCE: 5718-72
; CURRENT APPLICATION NUMBER: US/09/410,935B
; CURRENT FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/109,201
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 60/103,294
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Gene specific primer 1 for Gps-2
US-09-410-935B-6
Query Match 77.1% Score 16.2; DB 4; Length 32;
Best Local Similarity 85.7% Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 CAGCAGCAGAGCTCTCATCAT 21
Db 3 CAGCAGCAGAGCTCTCATCAT 23
RESULT 2
US-07-885-689A-7
; Sequence 7, Application US/07885689A
; Patent No. 536876
; GENERAL INFORMATION:
; APPLICANT: Cho, Joong M.
; APPLICANT: Lee, Tae H.
; APPLICANT: Chung, Hyun H.
; APPLICANT: Lee, Yong B.
; APPLICANT: Lee, Tae G.
; APPLICANT: Park, Young W.
; APPLICANT: Han, Kyu B.
; TITLE OR INVENTION: Method for Production of Bovine Growth
; HORMONE Using a Synthetic Gene.
; NUMBER OF SEQUENCES: 38

```

CORRESPONDENCE ADDRESS:  
 ADDRESSER: Birch, Stewart, Kolash & Birch  
 STREET: P.O. Box 747  
 CITY: Falls Church  
 STATE: Virginia  
 COUNTRY: USA  
 ZIP: 22040-0747

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/885,689A  
 FILING DATE: 19-MAY-1992  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Svensson, Leonard R.  
 REGISTRATION NUMBER: 30,330  
 REFERENCE/DOCKET NUMBER: 377-144P  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-241-1300  
 TELEFAX: 703-241-2848  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 45 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 HYPOTHETICAL: NO  
 FEATURE:

NAME/KEY: 1.45  
 LOCATION: 1.45  
 OTHER INFORMATION: /label= oligonucleotide  
 OTHER INFORMATION: /note= "U7 oligonucleotide portion of synthetic  
 OTHER INFORMATION: BgH gene, Figure 1."

17-885-689A-7

Very Match 73.3%; Score 15.4; DB 1; Length 45;  
 Percent Local Similarity 94.1%; Pred. No. 2.5e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

4 CAGCAGAGTCTTCATCA 20  
 |||||  
 21 CAGCAGAGTCTTCACCA 37

UNT 3  
 8-467-603-35/c  
 Sequence 35, Application US/08467603  
 Patent No. 5843672

GENERAL INFORMATION:  
 APPLICANT: Morgenstern, Jay P.  
 APPLICANT: Kamieczny, Andrzej  
 APPLICANT: Bizindaukas, Christine B.  
 APPLICANT: Brauer, Andrew W.  
 TITLE OF INVENTION: Allergenic Proteins and  
 TITLE OF INVENTION: Peptides from Dog  
 TITLE OF INVENTION: Dander and Uses Therefor  
 NUMBER OF SEQUENCES: 104  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: LAHIVE & COCKFIELD  
 STREET: 60 State Street, suite 510  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII-text

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/467,603  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/156,549  
 FILING DATE:  
 APPLICATION NUMBER: 07/999,712  
 FILING DATE: 31-Dec-92  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragouras, Amy E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: IMI-026CP (IPC-048CP)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 227-5941  
 INFORMATION FOR SEQ ID NO: 35:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 31 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-467-603-35

Query Match 70.5%; Score 14.8; DB 2; Length 31;  
 Percent Local Similarity 88.9%; Pred. No. 4.3e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCTTCATC 19  
 |||||  
 Db 24 AGCAGCAGAGTCTTCATC 7

RESULT 4  
 US-08-466-793-35/c  
 Sequence 35, Application US/08466793  
 Patent No. 5891716

GENERAL INFORMATION:  
 APPLICANT: Morgenstern, Jay P.  
 APPLICANT: Kamieczny, Andrzej  
 APPLICANT: Bizindaukas, Christine B.  
 APPLICANT: Brauer, Andrew W.  
 TITLE OF INVENTION: Allergenic Proteins and  
 TITLE OF INVENTION: Peptides from Dog  
 TITLE OF INVENTION: Dander and Uses Therefor  
 NUMBER OF SEQUENCES: 104  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: LAHIVE & COCKFIELD  
 STREET: 60 State Street, suite 510  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII-text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/466,793  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/156,549  
 FILING DATE: 22-NOV-1993  
 APPLICATION NUMBER: 07/999,712  
 FILING DATE: 31-Dec-92  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragouras, Amy E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: IMI-026CP (IPC-048CP)  
 TELECOMMUNICATION INFORMATION:

2 AGCAGCAGTCTTCATC 19

FILE REFERENCE: 5206.200-US  
CURRENT APPLICATION NUMBER: US/09/110,959A

CURRENT FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 0822/97  
 PRIOR FILING DATE: 1997-07-07  
 PRIOR APPLICATION NUMBER: 1213/97  
 PRIOR FILING DATE: 1997-10-24  
 PRIOR APPLICATION NUMBER: 60/054,039  
 PRIOR FILING DATE: 1997-07-28  
 PRIOR APPLICATION NUMBER: 60/063,694  
 PRIOR FILING DATE: 1997-10-28  
 NUMBER OF SEQ ID NOS: 14  
 SOFTWARE: FaetsEQ for Windows Version 4.0  
 30 ID NO 11  
 LENGTH: 44  
 TYPE: DNA  
 ORGANISM: Bacillus sp.  
 39-110-959A-11

Very Match 69.5%; Score 14.6; DB 3; Length 44;  
 Best Local Similarity 81.0%; Pred. No. 5.6e+02;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATC 21  
 12 CAGCAGCAGCAGCTTCATC 32

LT 8  
 39-205-860-3  
 Sequence 3, Application US/09205860  
 Patent No. 5981732  
 INVENTOR: Lex M. Cowe  
 APPLICANT: Lex M. Cowe  
 TITLE OF INVENTION: ANTISENSE MODULATION OF 6-ALPHA-13 EXPRESSION  
 FILE REFERENCE: RTS-0031  
 CURRENT APPLICATION NUMBER: US/09/205,860  
 CURRENT FILING DATE: 1998-12-04  
 NUMBER OF SEQ ID NOS: 87  
 30 ID NO 3  
 LENGTH: 20  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: PCR Primer  
 39-205-860-3

Very Match 67.6%; Score 14.2; DB 2; Length 20;  
 Best Local Similarity 84.2%; Pred. No. 7.6e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATC 19  
 2 CAGCAGCAGAGTCTTCAC 20

LT 9  
 39-657-452A-163  
 Sequence 163, Application US/09657452A  
 Patent No. 6426188  
 INVENTOR: Jacquesline Wate  
 APPLICANT: Bret P. Monia  
 TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHORYLASE KINASE ALPHA 1 EXPRESSION  
 FILE REFERENCE: RTS-0125  
 CURRENT APPLICATION NUMBER: US/09/657,452A  
 CURRENT FILING DATE: 2000-09-07  
 NUMBER OF SEQ ID NOS: 178  
 30 ID NO 163  
 LENGTH: 20  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: Antisense Oligonucleotide  
 39-657-452A-163

Query Match 67.6%; Score 14.2; DB 4; Length 20;  
 Best Local Similarity 84.2%; Pred. No. 7.6e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATC 19  
 DB 2 CATCATCATGCTTCATC 20

RESULT 10  
 US-09-360-545-57/c  
 Sequence 57, Application US/09360545  
 Patent No. 6429014  
 GENERAL INFORMATION:  
 APPLICANT: Croteau, Rodney B  
 APPLICANT: Bohlmann, Jorg  
 APPLICANT: Steele, Christopher L  
 APPLICANT: Phillips, Michael A  
 TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)  
 FILE REFERENCE: wau-13885  
 CURRENT APPLICATION NUMBER: US/09/360,545  
 CURRENT FILING DATE: 1999-07-26  
 EARLIER APPLICATION NUMBER: 60/052,249  
 EARLIER FILING DATE: 1997-11-07  
 EARLIER APPLICATION NUMBER: PCT/US98/14528  
 EARLIER FILING DATE: 1998-07-10  
 NUMBER OF SEQ ID NOS: 107  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 57  
 LENGTH: 24  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence:  
 OTHER INFORMATION: oligonucleotide corresponding to amino acid  
 OTHER INFORMATION: sequence set forth in SEQ ID NO:46  
 NAME/KEY: misc feature  
 LOCATION: (1)-(24)  
 OTHER INFORMATION: oligonucleotide that corresponds to the conserved  
 OTHER INFORMATION: amino acid sequence set forth in SEQ ID NO:46  
 US-09-360-545-57

Query Match 67.6%; Score 14.2; DB 4; Length 24;  
 Best Local Similarity 84.2%; Pred. No. 7.8e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATC 19  
 DB 24 CAGCAGCAGAGTCTTCAC 6

RESULT 11  
 US-09-130-663-10/c  
 Sequence 10, Application US/09130663A  
 Patent No. 6020163  
 GENERAL INFORMATION:  
 APPLICANT: Conklin, Darrell C.  
 TITLE OF INVENTION: LIPOCALIN HOMOLOG  
 FILE REFERENCE: 97-24  
 CURRENT APPLICATION NUMBER: US/09/130,663A  
 CURRENT FILING DATE: 1998-08-05  
 EARLIER APPLICATION NUMBER: 60/054,867  
 EARLIER FILING DATE: 1997-08-06  
 NUMBER OF SEQ ID NOS: 30  
 SOFTWARE: FaetsEQ for Windows Version 3.0  
 SEQ ID NO 10  
 LENGTH: 30  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: Oligonucleotide primer: ZC13270  
 39-657-452A-163





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EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
EO ID NO 3015
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-21687-313 : polymorphic base G or A
99-422-978-3015

Very Match          67.6%; Score 14.2; DB 4; Length 47;
1st Local Similarity 76.2%; Pred. No. 8.5e+02;
Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTTCATCAT 21
||| | ||| ||| ||| |||
35 CAGATCAGAGCTTTCATCTT 15

```





APPLICANT: Barbour, Eric  
 APPLICANT: Bucalire Meyer, Terry  
 APPLICANT: Bid Saad, Mohammed  
 TITLE OF INVENTION: No. US20030097690A1el Maize Promoters  
 FILE REFERENCE: 5718-72  
 CURRENT APPLICATION NUMBER: US/10/278,255  
 CURRENT FILING DATE: 2002-10-23  
 PRIOR APPLICATION NUMBER: US/09/410,935  
 PRIOR FILING DATE: 1999-10-04  
 PRIOR APPLICATION NUMBER: US 60/107,201  
 PRIOR FILING DATE: 1998-11-05  
 PRIOR APPLICATION NUMBER: US 60/103,294  
 PRIOR FILING DATE: 1998-10-06  
 NUMBER OF SEQ ID NOS: 19  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 6

LENGTH: 32  
 TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Gene specific primer 1 for Gcs-2  
 3-10-278-255-6

Query Match 77.1%; Score 16.2; DB 14; Length 32;  
 Best Local Similarity 85.7%; Pred. No. 3.2e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTTCATCAT 21  
 |||||  
 3 CAGCAGCAGAGCTTTCATCAT 23

RESULT 7

Sequence 43, Application US/10007010  
 Publication No. US2003012275A1

GENERAL INFORMATION:

APPLICANT: Alexander H. Borchers

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF HCK EXPRESSION

FILE REFERENCE: RTS-0345

CURRENT APPLICATION NUMBER: US/10/007,010

CURRENT FILING DATE: 2001-12-04

NUMBER OF SEQ ID NOS: 87

SEQ ID NO 43

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide  
 -10-007-010-43

Query Match 70.5%; Score 14.8; DB 14; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 1.4e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

3 GCAGCAGAGCTTTCATCA 20  
 |||||  
 1 GCTGACAGAGTTTCATCA 18

SULT 8

-09-944-326-1

Sequence 1, Application US/09944326

Patent No. US20020128220A1

GENERAL INFORMATION:

APPLICANT: Gleave, Martin

APPLICANT: Remle, Paul S.

APPLICANT: Miyake, Hideaki

APPLICANT: Nelson, Colleen

TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY

FILE REFERENCE: UBC.P-020-2

CURRENT APPLICATION NUMBER: US/09/944,326

CURRENT FILING DATE: 2001-08-30  
 PRIOR APPLICATION NUMBER: 60/121,726  
 PRIOR FILING DATE: 1999-02-26  
 PRIOR APPLICATION NUMBER: 09/913,325  
 PRIOR FILING DATE: 2001-08-10  
 NUMBER OF SEQ ID NOS: 14  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 1  
 LENGTH: 21  
 TYPE: DNA  
 ORGANISM: Murine  
 FEATURE:  
 OTHER INFORMATION: antisense TRPM-2 ODN  
 US-09-944-326-1

Query Match

70.5%; Score 14.8; DB 10; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 1.4e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTTCAT 18  
 |||||  
 Db 4 CAGCAGCAGAGATCTTCAT 21

RESULT 9

US-09-944-326-2

Sequence 2, Application US/09944326

Patent No. US20020128220A1

GENERAL INFORMATION:

APPLICANT: Gleave, Martin

APPLICANT: Remle, Paul S.

APPLICANT: Miyake, Hideaki

APPLICANT: Nelson, Colleen

TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY

FILE REFERENCE: UBC.P-020-2

CURRENT APPLICATION NUMBER: US/09/944,326

CURRENT FILING DATE: 2001-08-30

PRIOR APPLICATION NUMBER: 60/121,726

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: 09/913,325

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 21

TYPE: DNA

ORGANISM: Murine

FEATURE:

OTHER INFORMATION: mismatch control  
 US-09-944-326-2

Query Match

70.5%; Score 14.8; DB 10; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 1.4e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTTCAT 18  
 |||||  
 Db 4 CAGCAGCAGAGATCTTCAT 21

RESULT 10

US-09-967-726A-1

Sequence 1, Application US/0996726A

Publication No. US20030158130A1

GENERAL INFORMATION:

APPLICANT: Gleave, Martin

APPLICANT: Remle, Paul S.

APPLICANT: Miyake, Hideaki

APPLICANT: Nelson, Colleen

APPLICANT: Zellweger, Tobias

TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2

FILE REFERENCE: UBC.P-022

CURRENT APPLICATION NUMBER: US/09/944,326

CURRENT APPLICATION NUMBER: US/09/967,726A  
CURRENT FILING DATE: 2001-09-28  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 21  
TYPE: DNA  
ORGANISM: human  
-09-967-726A-1

Query Match 70.5%; Score 14.8; DB 12; Length 21;  
Best Local Similarity 88.9%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCAT 18  
|||||  
4 CAGCAGCAGAGTCTTCAT 21

ULT 11  
-09-967-726A-2  
Sequence 2, Application US/09967726A  
Publication No. US20030158130A1  
GENERAL INFORMATION:

APPLICANT: Gleave, Martin  
APPLICANT: Rennie, Paul S.  
APPLICANT: Miyake, Hideaki  
APPLICANT: Nelson, Colleen  
APPLICANT: Zellweger, Tobias  
TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2  
TITLE OF INVENTION: Oligonucleotides  
FILE REFERENCE: UBC-P-022  
CURRENT APPLICATION NUMBER: US/09/967,726A  
CURRENT FILING DATE: 2001-09-28  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2

LENGTH: 21  
TYPE: DNA  
ORGANISM: human  
-09-967-726A-2

Query Match 70.5%; Score 14.8; DB 12; Length 21;  
Best Local Similarity 88.9%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCAT 18  
|||||  
4 CAGCAGCAGAGTCTTCAT 21

ULT 12  
-10-080-794-1  
Sequence 1, Application US/10080794  
Publication No. US2003016591A1  
GENERAL INFORMATION:

APPLICANT: Rennie, Martin  
APPLICANT: Gleave, Paul S.  
APPLICANT: Miyake, Hideaki  
APPLICANT: Nelson, Colleen  
APPLICANT: Monia, Brett P.  
TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE  
TITLE OF INVENTION: HAVING 2'-O-(2-METHOXY)ETHYL MODIFICATIONS  
FILE REFERENCE: UBC-P-020-3  
CURRENT APPLICATION NUMBER: US/10/080,794  
CURRENT FILING DATE: 2002-02-22  
PRIOR APPLICATION NUMBER: 60/121,726  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 09/913,325  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 09/944,326  
PRIOR FILING DATE: 2001-08-30  
NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Murine  
FEATURE:  
OTHER INFORMATION: antisense TRPM-2 ODN  
US-10-080-794-1

Query Match 70.5%; Score 14.8; DB 12; Length 21;  
Best Local Similarity 88.9%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCAT 18  
|||||  
Db 4 CAGCAGCAGAGTCTTCAT 21

RESULT 13

US-10-080-794-2  
Sequence 2, Application US/10080794  
Publication No. US2003016591A1  
GENERAL INFORMATION:

APPLICANT: Gleave, Martin  
APPLICANT: Rennie, Paul S.  
APPLICANT: Miyake, Hideaki  
APPLICANT: Nelson, Colleen  
APPLICANT: Monia, Brett P.  
TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE  
TITLE OF INVENTION: HAVING 2'-O-(2-METHOXY)ETHYL MODIFICATIONS  
FILE REFERENCE: UBC-P-020-3  
CURRENT APPLICATION NUMBER: US/10/080,794  
CURRENT FILING DATE: 2002-02-22  
PRIOR APPLICATION NUMBER: 60/121,726  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 09/913,325  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 09/944,326  
PRIOR FILING DATE: 2001-08-30  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2

LENGTH: 21  
TYPE: DNA  
ORGANISM: Murine  
FEATURE:  
OTHER INFORMATION: mismatch control  
US-10-080-794-2

Query Match 70.5%; Score 14.8; DB 12; Length 21;  
Best Local Similarity 88.9%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCAT 18  
|||||  
Db 4 CAGCAGCAGAGTCTTCAT 21

RESULT 14

US-09-374-671-35/c  
Sequence 35, Application US/09374671  
Patent No. US20020012963A1  
GENERAL INFORMATION:

APPLICANT: Morgenstern, Jay P.  
APPLICANT: Kanieczny, Andrzej  
APPLICANT: Bizindauskas, Christine B.  
APPLICANT: Brauer, Andrew W.  
TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog  
TITLE OF INVENTION: Dander and Uses Therefor  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIRV & COCKFIELD, LLP  
STREET: 28 State Street

us-09-944-326-4.11m.rnpb

CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII-text

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/374,671  
FILING DATE:

CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/491,861  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Mandragoras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 742-4214  
TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: cDNA

I-09-374-671-35

Query Match 70.5%; Score 14.8; DB 9; Length 31;  
Best Local Similarity 88.9%; Pred. No. 1.5e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 AGACGAGAGCTTTCATC 19  
||| ||| ||| ||| |||  
24 AGACGAGAGCTTTCATC 7

SUBT 15  
Sequence 35, Application US/10196107A  
Publication No. US20030049691A1  
GENERAL INFORMATION:  
APPLICANT: Morgenstern, Jay P.  
Komieczny, Andrzej  
Bisindukas, Christine B.  
Brueer, Andrew W.

TITLE OF INVENTION: Allergenic Protein and Peptides from Dog  
Dander and Uses Therefor

NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Lahive & Cockfield, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII text

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/196,107A  
FILING DATE: 16-Jul-2002

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/374,671  
FILING DATE: 1999-AUG-16  
APPLICATION NUMBER: US 08/491,861  
FILING DATE: 1995-OCT-27

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? APPLICATION NUMBER: PCT/US93/12468
? FILING DATE: 1993-DEC-30
? APPLICATION NUMBER: US 08/156,549
? FILING DATE: 1993-NOV-22
? APPLICATION NUMBER: US 07/999,712
? FILING DATE: 1992-DEC-31
ATTORNEY/AGENT INFORMATION:
NAME: DiGiorgio, Jeanne M.
REGISTRATION NUMBER: 41,710
REFERENCE/DOCKET NUMBER: IM1-026C2CNCPCADV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 743-4214
? INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-196-107A-35

Query Match          70.5%; Score 14.8; DB 14;
Best Local Similarity 88.9%; Pred. No. 1.Se+03;
Matches      16; Conservative    0; Mismatches      2;

      2 AGACGAGAGTTCATC 19
      |||||||
Db   24 AGACGACGGTTCATC 7

```

```

Oy      2 AGCAGCAGAGCTTCATC 19
        |||||||
Db      24 AGCAGCAGAGCTTCATC 7

Query Match      70.5%; Score 14.8; DB 14; Length 31;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Search completed: November 8, 2003, 04:48:00
Job time : 241 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

4 nucleic - nucleic search, using sw model

on on: November 8, 2003, 00:42:33 ; Search time 2054 Seconds  
(without alignments)  
248.488 Million cell updates/sec

File: US-09-944-326-4

Perfect score: 21

Sequence: 1 cagcagcagagctcctcatcat 21

Sorting table: IDENTITY NUC  
Gapop 10.0, Gapexc 1.0

Marched: 22781392 segs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database:

EST.\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_estro:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est4:\*  
13: gb\_est5:\*  
14: gb\_est6:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_g88\_hum:\*  
18: em\_g88\_inv:\*  
19: em\_g88\_pln:\*  
20: em\_g88\_vit:\*  
21: em\_g88\_fun:\*  
22: em\_g88\_man:\*  
23: em\_g88\_mus:\*  
24: em\_g88\_pro:\*  
25: em\_g88\_rtd:\*  
26: em\_g88\_phg:\*  
27: em\_g88\_vit:\*  
28: gb\_g881:\*  
29: gb\_g882:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	21	100.0	85	9	AM276802 xp66a01.x
2	21	100.0	100	10	BP920141
3	21	100.0	102	10	BP958934
4	21	100.0	119	10	AM901233

C	5	21	100.0	124	12	BM821731	BM821731 K-EST0090
C	7	21	100.0	138	13	BQ339862	BQ339862 PM1-NN120
C	8	21	100.0	142	14	D45267	D45267 HUMG1194 H
C	9	21	100.0	147	13	BQ339466	BQ339466 PM1-NN120
C	10	21	100.0	148	10	BP846357	BP846357 PM1-EN006
C	11	21	100.0	149	14	R47195	R47195 CBS-38 Sub
C	12	21	100.0	169	10	BE76895	BE76895 RC2-NT011
C	13	21	100.0	177	9	AL048592	AL048592 DKF2P586H
C	14	21	100.0	183	12	BI032792	BI032792 MR4-NN018
C	15	21	100.0	184	10	BP958930	BP958930 PM1-NN120
C	16	21	100.0	185	12	BI036860	BI036860 MR4-NT014
C	17	21	100.0	196	9	A1745406	A1745406 wcl341.x
C	18	21	100.0	197	12	BI036862	BI036862 MR4-NT014
C	19	21	100.0	201	10	BP957666	BP957666 PM1-NN120
C	20	21	100.0	203	10	BP957653	BP957653 PM1-NN120
C	21	21	100.0	207	10	BP957858	BP957858 PM1-NN120
C	22	21	100.0	224	9	AM161224	AM161224 aut0a10.Y
C	23	21	100.0	226	10	BF951119	BF951119 MR4-NT014
C	24	21	100.0	236	10	BP948789	BP948789 MR3-NN021
C	25	21	100.0	238	10	BF923639	BF923639 MR4-NT014
C	26	21	100.0	243	9	AA336628	AA336628 EST1242
C	27	21	100.0	244	10	BE766870	BE766870 RC2-NT011
C	28	21	100.0	248	10	BF923643	BF923643 MR4-NT014
C	29	21	100.0	249	10	BP945175	BP945175 PM1-NN120
C	30	21	100.0	250	13	BQ345410	BQ345410 MR4-NT014
C	31	21	100.0	252	10	BF923633	BF923633 MR4-NT014
C	32	21	100.0	252	10	BF963107	BF963107 PM1-NN120
C	33	21	100.0	253	10	BF887875	BF887875 OV2-TN017
C	34	21	100.0	253	12	BI041998	BI041998 MR4-NT014
C	35	21	100.0	256	12	BI041248	BI041248 MR4-NT014
C	36	21	100.0	258	10	BP961150	BP961150 PM1-NN120
C	37	21	100.0	262	10	BP947155	BP947155 MR3-NN021
C	38	21	100.0	262	13	BQ339859	BQ339859 PM1-NN120
C	39	21	100.0	263	10	BE899032	BE899032 601682590
C	40	21	100.0	265	10	BP961152	BP961152 PM1-NN120
C	41	21	100.0	268	10	BP920149	BP920149 MR1-NT017
C	42	21	100.0	269	10	BP948799	BP948799 MR3-NN021
C	43	21	100.0	269	13	BQ339911	BQ339911 MR3-NN021
C	44	21	100.0	272	10	BP956582	BP956582 PM1-NN120
C	45	21	100.0	273	10	BP947794	BP947794 MR3-NN021

## ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION  
AM276802 xp66a01.x1 NCI CGAP OV39 Homo sapiens CDNA clone IMAGE:2745288 3'  
similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN); mRNA sequence.  
AM276802  
VERSION  
AM276802.1 GI:6663832  
KEYWORDS  
EST.  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
1 (bases 1 to 85)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Andrew Berchuck M.D., John Gillespie M.D.,  
Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: David B. Kitzman, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/BLINL at:  
[www.bio.lnlnl.gov/bdrp/image/image.html](http://www.bio.lnlnl.gov/bdrp/image/image.html)



Possible reversed clone: polyT not found  
Seq primer: -40UP from Gibco.  
Location/Qualifiers

1. .85

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2745288"

/sex="female"

/tissue\_type="papillary serous ovarian metastasis"

/clone\_id="NCI\_CGAP-Ov39"

/note="Organ: ovary; Vector: PAMP10; cDNA made by oligo-dT priming. Non-directionally cloned into the UNG sites of PAMP10. Size-selected on agarose gel, average insert size 500 bp. Primary library; non-amplified. cDNA library preparation: David B. Krizman, Ph.D (NCI). Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

18 COUNT 18 a 21 c 30 g 16 t

Query Match 100.0%; Score 21; DB 9; Length 85;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGGCTTCATCAT 21  
82 CAGCAGCAGGCTTCATCAT 62

BP920141 100 bp mRNA linear EST 19-JAN-2001  
PM1-NT0179-071100-003-f02 NT0179 Homo sapiens cDNA, mRNA sequence.  
BP920141 GI:12316029  
EST.  
Homo sapiens (human)  
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 100)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,  
M.U., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800

CONTACT: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?fl=PM1&lc2=PM1-NT0179-  
071100-003-f02&lc3=2000-11-07&lc4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 11  
High quality sequence stop: 100.  
Location/Qualifiers

1. .100  
/organism="Homo sapiens"

/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_id="NT0179"  
/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORSSTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

BASE COUNT 21 a 34 c 20 g 25 t  
ORIGIN  
Query Match 100.0%; Score 21; DB 10; Length 100;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGGCTTCATCAT 21  
56 CAGCAGCAGGCTTCATCAT 76

BP958934 102 bp mRNA linear EST 22-JAN-2001  
PM1-NN1200-011200-009-b07 NN1200 Homo sapiens cDNA, mRNA sequence.  
BP958934 GI:12376209  
EST.  
Homo sapiens (human)  
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 102)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,  
M.U., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800

CONTACT: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?fl=PM1&lc2=PM1-NN1200-  
011200-009-b07&lc3=2000-12-01&lc4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 11  
High quality sequence stop: 101.  
Location/Qualifiers

1. .102  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_id="NN1200"  
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORSSTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of

Query Match 100.0%; Score 21; DB 10; Length 102;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTTCATCAT 21  
 |||||  
 91 CAGCAGCAGAGCTTTCATCAT 71

RESULT 4  
 1901233/c 119 bp mRNA linear EST 24-MAY-2000

DEFINITION CM4-NN1011-100300-110-g04 NN1011 Homo sapiens cDNA, mRNA sequence.

ACCESSION AM901233.1 GI:8065542

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 119)

AUTHORS Das Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Ngai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

M.J., Soares, F., Brenham, R.K., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

10737800

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Query Match 100.0%; Score 21; DB 10; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTTCATCAT 21  
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 103 CAGCAGCAGAGCTTTCATCAT 83

RESULT 5  
 BM821731 124 bp mRNA linear EST 06-MAR-2002

DEFINITION K-EST0090952 S20T665307 Homo sapiens cDNA clone S20T665307-15-H01

ACCESSION BM821731

VERSION BM821731.1 GI:19178144

KEYWORDS Homo sapiens (human)

SOURCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 124)

AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,

Oh, K.J., Cheong, J.B., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and

Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Beom-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 15 row: H column: 01

High quality sequence stop: 124.

Location/Qualifiers

1. 124

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

BASE COUNT 27 a 30 c 46 g 21 t

Query Match 100.0%; Score 21; DB 12; Length 124;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTTCATCAT 21  
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 102 CAGCAGCAGAGCTTTCATCAT 82

RESULT 6  
 BQ339862 138 bp mRNA linear EST 20-MAY-2002

DEFINITION BQ339862

PM1-NN1200-011200-010-f07 NN1200 Homo sapiens cDNA, mRNA sequence.

ACCESSION BQ339862

VERSION BQ339862.1

KEYWORDS Homo sapiens (human)

SOURCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 138)

AUTHORS BQ339862

PM1-NN1200-011200-010-f07 NN1200 Homo sapiens cDNA, mRNA sequence.

Unpublished

Contact: BQ339862

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Beom-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 15 row: H column: 01

High quality sequence stop: 124.

Location/Qualifiers

1. 124

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

SESSION B0339862 GI:20999978  
 REGION EST.  
 WORDS Homo sapiens (human)  
 ORC Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 138)  
 Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F.,  
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,  
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
 Simpson, A.J.  
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 PUBMED 10737800  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the PAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&c2=PM1-NN1200-  
 011200-010-f07&c3=2000-12-01&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 17  
 High quality sequence stop: 35.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /def\_stages="Adult"  
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 Site 2: Sma1; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."  
 E COUNT 29 a 33 c 50 g 26 t  
 GIN  
 Query Match 100.0%; Score 21; DB 13; Length 138;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 CAGCAGCAGAGCTTCATCAT 21  
 |||||  
 127 CAGCAGCAGAGCTTCATCAT 107

TITLE High-density cDNA filter analysis of the expression profiles of the  
 JOURNAL gene preferentially expressed in human brain  
 MEDLINE Gene 164, 219-227 (1995)  
 PUBMED 96069586  
 COMMENT Contact: Nobuaki Takahashi  
 Institute of Medical Science  
 University of Tokyo  
 Shirokanedai 4-6-1, Minato-ku, Tokyo, Japan 108  
 Tel: 03-5449-5625  
 Fax: 03-5449-5445.  
 FEATURES  
 source  
 1..142  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Human cerebral cortex"  
 /note="Adult male cerebral cortex tissue."  
 BASE COUNT 26 a 31 c 55 g 30 t  
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 Query Match 100.0%; Score 21; DB 14; Length 142;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 CAGCAGCAGAGCTTCATCAT 21  
 |||||  
 79 CAGCAGCAGAGCTTCATCAT 59  
 RESULT 8  
 LOCUS B0339466 147 bp mRNA linear EST 20-MAY-2002  
 DEFINITION PM1-NN1200-051100-004-h12 NN1200 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION B0339466  
 VERSION B0339466.1 GI:20999152  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 147)  
 Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F.,  
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,  
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
 Simpson, A.J.  
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 PUBMED 10737800  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the PAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&c2=PM1-NN1200-  
 051100-004-h12&c3=2000-11-05&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 14  
 High quality sequence stop: 34.  
 Location/Qualifiers  
 1..147  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"

/dev\_stage="Adult"  
/clone\_lib="NM1200"  
/note="Organ: nervous normal; Vector: puc18; Site 1: Sma1;  
Site 2: Sma1; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
ASB COUNT 35 a 46 c 28 g 38 t  
RIGIN

Query Match 100.0%; Score 21; DB 13; Length 147;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 CAGCAGCAGAGCTTCATCAT 21  
122 CAGCAGCAGAGCTTCATCAT 142

RESULT 9  
XUS 7846357 148 bp mRNA linear EST 16-JAN-2001  
DEFINITION BF846357  
XBASES BF846357.1 GI:12233611  
XWORDS EST.  
XORCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 148)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Bioness, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordini, S., Costa, F.P.,  
Goldman, G.H., Carvalho, A.F., Matukuma, A., Bata, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,  
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 2020263  
PUBMED 10737800  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the PAPSP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM1&t2=PM1-EN0065-  
231000-002-b01&t3=2000-10-23&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 110.  
location/Qualifiers  
1. 148  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="EN0065"  
/note="Organ: lung; normal; Vector: puc18; Site 1: Sma1;  
Site 2: Sma1; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

ATUES  
source

38 COUNT  
24 a 56 c 41 g 27 t

ORIGIN  
Query Match 100.0%; Score 21; DB 10; Length 148;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 CAGCAGCAGAGCTTCATCAT 21  
34 CAGCAGCAGAGCTTCATCAT 54  
DB

RESULT 10  
R47195/c 149 bp mRNA linear EST 12-DEC-1995  
LOCUS CBS-389 Subtractive cDNA library, ocular ciliary body Homo sapiens  
DEFINITION CBS-389 5' end similar to TRPM-2 (clusterin) (accession  
number M64722), mRNA sequence.  
R47195  
R47195.1 GI:807537  
EST.  
XBASES R47195  
XWORDS EST.  
XORCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 149)  
Escarbano, J., Ortega, J. and Coca-Prados, M.  
TITLE Isolation and characterization of cell-specific cDNA clones from a  
subtractive library of the ocular ciliary body of a single normal  
human donor: Transcription and synthesis of plasma proteins  
J. Biochem. 118 (5), 921-931 (1995)  
MEDLINE 96318503  
PUBMED 8749308

COMMENT Contact: Coca-Prados, M.  
Department of Ophthalmology and Visual Science  
Yale University Medical School  
330 Cedar Street, New Haven, CT 06520-8061  
Tel: 2037852742  
Fax: 2037856123  
Email: mguel.coca-prados@quickmail.yale.edu  
Seq primer: T3.  
location/Qualifiers  
1. 149  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="CBS-389"  
/note="Vector: Bluescript II SK; Site 1: EcoRI; Site 2:  
hybridizing antisense, single-stranded phagemid DNA (ssDNA  
) (as pBluescript SK-) from the ocular ciliary body cDNA  
library (target) of a 34-year-old female donor in  
lambda-Uni-ZAP XR with biotinylated sense RNA of an ocular  
cell line cDNA library (driver) in the same vector."

FEATURES  
source

BASE COUNT 33 a 31 c 56 g 29 t  
ORIGIN  
Query Match 100.0%; Score 21; DB 14; Length 149;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 CAGCAGCAGAGCTTCATCAT 21  
71 CAGCAGCAGAGCTTCATCAT 51  
DB

RESULT 11  
BE766895/c 169 bp mRNA linear EST 19-SEP-2000  
DEFINITION RC2-NT0110-050600-013-f03 NT0110 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BE766895  
VERSION BE766895.1 GI:10196619  
KEYWORDS EST.

**ORIGIN** Homo sapiens (human)  
**ORIGIN** Homo sapiens  
**REFERENCE** Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 169)  
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
**TITLE** Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
**EDLINE** 20202663  
**PUBMED** 10737800  
**COMMENT** Contact: Simpson, A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=RC2-WT0110-050  
 600-013-f036ct3-2000-06-05&rt=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 18  
 High quality sequence stop: 169.  
**FEATURES**  
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 1. 169  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="NT0110"  
 /note="Organ: nervous tumor; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
**BASE COUNT**  
 GIN 37 a 36 c 59 g 37 t  
**Query Match** 100.0%; Score 21; DB 10; Length 169;  
 Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 CAGCAGCAGAGCTTCATCAT 21  
 ||||||||||||||||||||  
 59 CAGCAGCAGAGCTTCATCAT 39  
**TITLE** AL048592 177 bp mRNA linear EST 01-MAR-2000  
**JOURNAL** DKFZ586H092\_r1 586 (synonym: hute1) Homo sapiens cDNA clone  
**EDLINE** DKFZ586H092, mRNA sequence.  
**PUBMED** AL048592  
**COMMENT** EST.  
 AL048592.1 GI:4729143  
**ORIGIN** Homo sapiens (human)  
**ORIGIN** Homo sapiens  
**REFERENCE** Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 177)  
 Pousetka, A., Klein, M., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
**TITLE** Unpublished

**COMMENT**  
 Contact: Pousetka A.J.  
 Department Leinrach  
 Max-Planck-Institute for Molecular Genetics  
 Ihnestrasse 73, 14195 Berlin, Germany  
 Tel: +49-30-84131623  
 Fax: +49-30-84131128  
 Email: pousetka@mpg-berlin-dahlem.mpg.de  
 This is the 5' sequence of the clone insert  
 clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;  
 sequenced by DKFZ (German Cancer Research Center,  
 Heidelberg/Germany) within the cDNA sequencing consortium of the  
 German Genome Project.  
 No sequence available.  
 This clone (DKFZ586H092) is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
**FEATURES**  
 source  
 1. 177  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="DKFZ586H092"  
 /tissue\_type="uterus"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="DH10B"  
 /note="Vector: pSPori1, Site 1: NotI; Site 2: SalI/MluI"  
**BASE COUNT**  
 ORIGIN 40 a 41 c 64 g 32 t  
**Query Match** 100.0%; Score 21; DB 9; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 CAGCAGCAGAGCTTCATCAT 21  
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 77 CAGCAGCAGAGCTTCATCAT 57  
**RESULT** 13  
 B1032792 183 bp mRNA linear EST 14-JUN-2001  
**LOCUS** B1032792  
**DEFINITION** MR4-NN0188-220101-204-e01 NN0188 Homo sapiens cDNA, mRNA sequence.  
**ACCESSION** B1032792  
**VERSION** B1032792.1 GI:14439418  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORIGIN** Homo sapiens  
**ORIGIN** Homo sapiens  
**REFERENCE** Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 183)  
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
**TITLE** Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
**EDLINE** 20202663  
**PUBMED** 10737800  
**COMMENT** Contact: Simpson, A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=NR4&c2=NR4-NN0188-220101-204-e0&c3=2001-01-22&c4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 183.

## FEATURES

SOURCE

1. 183  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_1b="NN0188"  
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
BASE COUNT  
28 a 72 c 48 g 35 t  
GIGIN

Query Match 100.0%; Score 21; DB 12; Length 183;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21  
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69 CAGCAGCAGAGCTTCATCAT 89

:/SULF 14  
958930/c  
CUS BP958930 184 bp mRNA linear EST 22-JAN-2001  
FINITION PM1-NN1200-011200-009-g08 NN1200 Homo sapiens cDNA, mRNA sequence.  
CRSSION BP958930  
RSION BP958930.1 GI:12376205  
YWORDS  
URCR  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
Dias Neto, R., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL  
MEDLINE  
PUBMED  
20202663  
10737800

CONTACT: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&c2=PM1-NN1200-011200-009-g08&c3=2001-12-01&c4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 7  
High quality sequence stop: 184.  
Location/Qualifiers

## FEATURES

SOURCE

1. 184  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"

/dev\_stage="Adult"  
/clone\_1b="NN1200"  
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
BASE COUNT  
47 a 36 c 61 g 40 t  
ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 184;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21  
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46 CAGCAGCAGAGCTTCATCAT 26

RESULT 15  
BI036860 185 bp mRNA linear EST 14-JUN-2001  
LOCUS NR4-WT0140-080101-209-c09 NT0140 Homo sapiens cDNA, mRNA sequence.  
DEFINITION BI036860  
ACCESSION BI036860.1 GI:14443486  
VERSION  
KEYWORDS  
EST.  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
Dias Neto, R., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL  
MEDLINE  
PUBMED  
20202663  
10737800

CONTACT: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=NR4&c2=NR4-NT0140-080101-209-c09&c3=2001-01-08&c4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 17  
High quality sequence stop: 134.  
Location/Qualifiers

## FEATURES

SOURCE

1. 185  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
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/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BE COUNT 41 a 42 c 62 g 40 t  
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Query Match 100.0%; Score 21; DB 12; Length 185;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21  
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43 CAGCAGCAGAGTCTTCATCAT 23

Search completed: November 8, 2003, 01:25:51  
Time : 2057 secs